

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 16:26:16 ; Search time 395 Seconds
(without alignments)
8446.793 Million cell updates/sec

Title: US-09-367-052-1
Perfect score: 1877
Sequence: 1 ccatcttaatacactact.....aaaaaAAAAAAAAAAAA 1877

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 segs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/1_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974.4	51.9	1737	2	US-08-202-056-4
2	974.4	51.9	1737	2	US-08-076-093A-3
3	974.4	51.9	1737	2	US-08-701-265-3
4	974.4	51.9	1737	2	US-08-284-586-3
5	974.4	51.9	1737	2	US-08-805-478-3
6	974.4	51.9	1737	2	US-08-802-627A-3
7	974.4	51.9	1737	2	US-08-801-238-3
8	974.4	51.9	1737	2	US-08-801-228-3
9	974.4	51.9	1737	2	US-08-014-296-3
10	974.4	51.9	1737	6	PCT-US94-06380-2
11	952.8	50.8	1679	3	US-09-517-605-14
12	951.8	50.7	1664	3	US-09-582-224A-5
13	951.8	50.7	1664	3	US-09-023-655-1213
14	859	45.8	1225	3	US-09-016-434-1235
15	834.6	44.5	1317	2	US-08-153-848-45
16	834.6	44.5	1317	3	US-09-299-843A-45
17	834.6	44.5	1317	3	US-09-088-337B-45
18	834.6	44.5	1317	6	PCT-US93-11153-45
19	809.6	43.1	1059	3	US-09-647-501-1
20	804.8	42.9	1059	3	US-09-826-509-484
21	282	15.0	440	3	US-09-513-999C-1915
22	198.4	10.6	1119	3	US-09-170-496D-65
23	198.4	10.6	1679	2	US-08-202-056-4
24	198.4	10.6	1679	2	US-08-076-093A-5

25	198.4	10.6	1679	2	US-08-701-265-5	Sequence 5, Appli
26	198.4	10.6	1679	2	US-08-284-586-5	Sequence 5, Appli
27	198.4	10.6	1679	2	US-08-805-478-5	Sequence 5, Appli
28	198.4	10.6	1679	2	US-08-802-627A-5	Sequence 5, Appli
29	198.4	10.6	1679	2	US-08-801-238-5	Sequence 5, Appli
30	198.4	10.6	1679	2	US-08-801-228-5	Sequence 5, Appli
31	198.4	10.6	1679	3	US-09-104-296-5	Sequence 5, Appli
32	198.4	10.6	1679	6	PCT-US94-06380-3	Sequence 3, Appli
33	198.4	10.6	2802	3	US-09-949-016-4384	Sequence 4384, Ap
34	198.4	10.6	2818	3	US-08-982-493-7	Sequence 7, Appli
35	198.4	10.6	2818	3	US-08-628-655-1	Sequence 1, Appli
36	198.4	10.6	16404	3	US-09-949-016-16126	Sequence 16126, A
37	196.8	10.5	1119	3	US-09-170-496D-199	Sequence 199, App
38	195.8	10.4	2085	3	US-09-299-843A-65	Sequence 65, Appl
39	195.8	10.4	2085	3	US-09-088-337B-65	Sequence 65, Appl
40	193.8	10.3	1107	3	US-09-170-496D-19	Sequence 19, Appl
41	193.8	10.3	1293	3	US-09-016-434-1052	Sequence 1052, Ap
42	193.8	10.3	1670	3	US-08-709-838-1	Sequence 1, Appli
43	193.8	10.3	1670	3	US-08-829-839-1	Sequence 1, Appli
44	193.8	10.3	1670	3	US-09-023-655-980	Sequence 980, App
45	193.8	10.3	1670	3	US-09-624-594-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-202-056-4
; Sequence 4, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharpai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-202-056-4

Query Match

51.9%; Score 974.4; DB 2; Length 1737;

Best Local Similarity 76.1%; Pred. No. 1.1.2e-181; Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;		
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Db	20	GCAGGTAGCAGTGAACCTCTGAGGGCTTTGGTCTCGGTAAACACACGCGCTGTGAGC 79
QY	110	GAGTGTGGCATGGAACCGATCAGTGTGAGTATATACATCTTCGATGAACCTACCTCAAGA 169
Db	80	CAGCGTTTACATGGA-----GGGGATCAGTATATACATCTTCGATGAACCTACCTCAAGA 134
QY	170	AGTGGGGTCTGGAGCATATGACTCCAAAGAGAACCTCTCTCCGGGATGAAAACGTCCA 229
Db	135	AATGGGCTCAGGGGACTATGACTCCATGAAGGAACCTCTCTCCGGGATGAAAACGTCCA 194
QY	230	TTTCAATAGGATCTCTGCGCCACCATCTACTCTTCATCATCTCTTGAATGGCATATGCGG 289
Db	195	TTTCAATAGGATCTCTGCGCCACCATCTACTCTTCATCATCTCTTGAATGGCATATGCGG 254
QY	290	CAATGATTTGGTCACTCTGCTGATGGTTTACCAAGAGAACCTTAAGAGCATGACGACAA 349
Db	255	CAATGATTTGGTCACTCTGCTGATGGTTTACCAAGAGAACCTTAAGAGCATGACGACAA 314
QY	350	GTACCGGCTGCACCTGTGAGTGGCTGACCTCTCTTTGTTCATCACAATCCCTCTTCTGGGC 409
Db	315	GTACAGGCTGCACCTGTGAGTGGCTGACCTCTCTTTGTTCATCACAATCCCTCTTCTGGGC 374
QY	410	AGTTGATGCAATGGCTGACCTGTGAGTGGCTGACCTCTCTTTGTTCATCACAATCCCTCTT 469
Db	375	AGTTGATGCAATGGCTGACCTGTGAGTGGCTGACCTCTCTTTGTTCATCACAATCCCTCTT 434
QY	470	CTACAGTCTCAACCTCTACAGCAGCTTCTCATCTGGCCCTTCATCAGCCTGACCGGTA 529
Db	435	CTACAGTCTCAACCTCTACAGCAGCTTCTCATCTGGCCCTTCATCAGCCTGACCGGTA 494
QY	530	CTCGGCAATGTCCAGCCACCAACAGTCAAAGGCCAAAGAACTGCTGGCTGAAAAGGC 589
Db	495	CTCGGCAATGTCCAGCCACCAACAGTCAAAGGCCAAAGAACTGCTGGCTGAAAAGGC 554
QY	590	AGTCTATGTGGGGCTGTGATCCAGCCCTCTCTCTGATATATACCTGACCTTCTTTCG 649
Db	555	AGTCTATGTGGGGCTGTGATCCAGCCCTCTCTCTGATATATACCTGACCTTCTTCTTTCG 614
QY	650	CGAGCTCAGCGGGGACATCAGTCAAGGGGATGACAGTACATCTGTGACCGCTTTA 709
Db	615	CAAG-----TCAGTGAGGAGATGACAGATATATCTGTGACCGCTTTA 659
QY	710	CCCCGATAGCTGTGGATGGTGTGTTTCAATCCAGCATATATATGGTGGGTCTCATCTT 769
Db	660	CCCCAATGACTGTGGTGGTGTGTTTCAATCCAGCATATATATGGTGGGTCTCATCTT 719
QY	770	GCCCGGATCGTCACTCTCTCTGTTACTGTCATCATCTCTTAAGTGTCACTCCAA 829
Db	720	GCTGTGTATGTCATCTCTCTCTGTTACTGTCATCATCTCTTAAGTGTCACTCCAA 779
QY	830	GGGCCACCAAGAGCGCCCTCAAGACGACATCATCTCTAGCTTTCTTTTCG 889
Db	780	GGGCCACCAAGAGCGCCCTCAAGACGACATCATCTCTAGCTTTCTTTTCG 839
QY	890	CTGCTGGCTGCCATATATATGGGGATCAGCATCGACTCTCTTCTCTTTTGGGAGTCAT 949
Db	840	CTGTTGGCTGCCATATATATGGGGATCAGCATCGACTCTCTTCTCTTCTGGGAATCAT 899
QY	950	CAAGCAAGGATGACTTCCAGAGCATTTGGCAAGATGATGATCTCATCAAGAGCCCT 1009
Db	900	CAAGCAAGGATGACTTCCAGAGCATTTGGCAAGATGATGATCTCATCAAGAGCCCT 959
QY	1010	CGCTTTCTTCCATGTTGCTGAACCCCATCTCTATGCTTCTCTGGGGCCAAAGTTCAA 1069
Db	960	AGCTTTCTTCCATGTTGCTGAACCCCATCTCTATGCTTCTCTGGAGCCAAATTTAA 1019
QY	1070	AAGCTCTGCCAGCATGCACTCAACTCCATGAGCAGAGGCTCCAGGCTCAAGATCTCTTC 1129

Db	1020	AACCTCTGCCAGCAGCAGCACTCACTCTCTGTGAGCAGAGGGCTCCAGCCTCAAGATCTCTC 1079
QY	1130	CAAAGAAAGCGGGTGGACACTCTTCCGTCTCCCGAGGAGTCAGATCCTCCAGTTTTC 1189
Db	1080	CAAAGAAAGCGGGTGGACACTCTTCCGTCTCCCGAGGAGTCAGATCCTCCAGTTTTC 1139
QY	1190	CTCCAGCTAACCTTATGCAAGAGCTTATATATATATATATATATATATATATATATAT 1249
Db	1140	CTCCAGCTAA-----CACAGATCTAAAGAGCTTTTATATACGATAAATAACTTTT 1191
QY	1250	TTTTATGTTACACATTTTCCAGATATAAGAGACTGACCACTCTGTGACAGTTTTTTTT 1309
Db	1192	TTTTATGTTACACATTTTCCAGATATAAAGAGCTGACCAATATATGACAGTTTATATG 1251
QY	1310	TTTTTAAATGACCTGTGGGAGTTTATGTTCTCTAGTTTCTGAGGTTTGAGCTTAATTT 1369
Db	1252	TTGTTGGATTTTGT-----CTTGTGTTCTTTAGTTTGTGAAAGTTTAAATGACTTA 1305
QY	1370	ATATAAATATTTTGTCTTGTCTCATGTGAATGAGCGTCTTAGGCAGGACCTGTGGCC 1429
Db	1306	TTTATA-----TAAATTTTGTGTTTCATATTTGATGTGTCTAGGCAGGACCTGTGGCC 1361
QY	1430	AAGTCTTATGAGTGTGTTTATCTGTGTGAGGACTGTAGAACTGTGAGAGAAAGAACTGA 1489
Db	1362	AAGTCTTATGAGTGTGTTTATCTGTGTGAGGACTGTAGAA-----AAGGGAAGCTGA 1413
QY	1490	ACATTCAGCAATGTGTGTAATTTGAATTAAGCTAGCCGTGATCCTCAGCTGTGCTGCA 1549
Db	1414	ACATTCAGCAATGTGTGTAATTTGAATTAAGCTAGCAATGATCCCAAGCTGTGTTATGCA 1473
QY	1550	TAATCTCTTCTTCCGAGGAGCACCACCCACCCACCCACCCACCCACCCACCCACCTTT 1609
Db	1474	TAGATATCTCTCCA----- 1488
QY	1610	TGTTGGTTATGCTGTGTGATGGTTTGTGTTGTTTGTGTTGTTGTTGTTGTTT 1669
Db	1489	-----TTCCCGTGAAGCGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1525
QY	1670	TTTTCTGTAAGAGTGGCACTTAAACCAAGCGTGAATGCTGTAGAAATGCTGGGT 1729
Db	1526	TTTGTGTAAGAGTGGCACTTAAACCAAGCGTGAATGCTGTAGAAATGCTGGGT--- 1581
QY	1730	TTTTTTTGTGTTGTTGTTTCTTCAAGAGTAGATTGACTTTGAGTCCCTTCAAAAT 1789
Db	1582	-----TTTTTCAGTTTTCAGGAGTGGGTGATTTTCAGCACCCTAC-AGT 1623
QY	1790	GTACAGCTTTGATATACATGTTTAAATAAGTCAATGATAAACTTAAATAAAAAAAAAA 1849
Db	1624	GTACAGCTTTGATATGAGTTTAAATAAGTCAATGATAAACTTAAATAAAAAAAAAA 1683
QY	1850	AAAAAAAAAAAAAAAAAAAAAAAAA 1877
Db	1684	AAAAAAAAAAAAAAAAAAAAAAAAA 1711

RESULT 2
US-08-076-093A-3
; Sequence 3, Application US/08076093A
; Patent No. 5543503
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

Query Match	51.9%;	Score	974.4;	DB 2;	Length	1737;
Best Local Similarity	76.1%;	Pred. No.	1.2e-181;			
Matches 1391;	Conservative	0;	Mismatches	301;	Indels	136;
Gaps	10;					
QY	50	GCAGGTAGCAGTGCACCTCTGAGGCGGTTTCGGTGTCCGGTAAACACCAACCGCTGTACAGC	109			
Db	20	GCAGCGGCAAAAGTGACGCCGAGGGCTGAGTGCTCCAGTAGCCACCGCATCTGGAGAAC	79			
QY	110	GAGTGTTCATGGAAACCGATCAGTGTGAGTATATACACTTCTGTGATAACTCTCTGAAGA	169			
Db	80	CACGCGGTACCATGGA-----GGGGATCAGTATATACACTTTCAGATAACTACACCCGAGGA	133			
QY	170	AGTGGGCTCTGGAGACTATGACTCCAAACAGGAACCCCTGCTTCGGGATCAAAACGTCCTCA	229			
Db	135	AATGGGCTCAGGGGACTATGACTCCATGAAGGAACCCCTGTTCCGTGAAGAAATGCTAA	194			
QY	230	TTTCAATAGGATCTTCTGCGCCACCACTACTTCATCATCTCTTGTGATGGCATATGTCGG	289			
Db	195	TTTCAATAAAATCTTCTGCGCCACCACTACTCCATCATCTTCTTAACTGGCATTTGTGGG	254			
QY	290	CAATGGATTGGTCATCTCTGTCATGGGTACACAGAAGAACTAAGGAGCATGACGGACAA	349			
Db	255	CAATGGATTGGTCATCTCTGTCATGGGTACACAGAAGAACTGNAAGCATGACGGACAA	314			
QY	350	GTAACGGCTGCACCTGTTCAGTGCTGACCTCTCTTTGTTCATCACATCTCCCTTCTGGGC	409			
Db	315	GTAACGGCTGCACCTGTTCAGTGCGCGACCTCTCTTTGTTCATCACGCTTCTCTTCTGGGC	374			
QY	410	AGTTGATGCCATCGCTGACCTGTACTTTTGGAAATTTTGTGTGAAGGCTGTCCATATCAT	469			
Db	375	AGTTGATGCCGTGGCAAACTGTGTACTTTGGAACTTCTTATGACAGCATCCATGTTCAT	434			
QY	470	CTACATGTCAACCTCTTACAGACGGTTCTCATCTGGCCCTTCATCAGCTGGACCGGTA	529			
Db	435	CTACACAGTCAACCTCTTACAGCAGTGTCTTCATCTGGCCCTTCATCAGCTGGACCGGTA	494			
QY	530	CCTCGGCATTTGCCAGCCACCAACAGTCAAGGCCAAGGAACCTGCTGGCTGAAAGGC	589			
Db	495	CCTGGCCATCTGTCCAGCCACCAACAGTCAAGGCCAAGGAAGCTGTGTGCTGAAAGGT	554			
QY	590	AGTCTATGTGGGCGTCTGGATCCAGCCCTCTCTGACTATATACCTGACTTTCATCTTTGC	649			

QY 1730 TTTTGTGTTGTTGTTTTCAGTTTTCAGAGTAGATTGACTTCAGTCCCTACAAAT 1789
Db 1582 -----TTTTTCAGTTTTCAGGAGTGGGTGATTTCAGCACCTAC-AGT 1623
QY 1790 GTACAGCTTGTATTACATGTTTAATAAAGTCAATGATAAACTTAAAAAAGAAAAA 1849
Db 1624 GTACAGCTTGTATTAAAGTTGTTTAATAAAGTACATGTTTAAACTTAAAAAAGAAAAA 1683
QY 1850 AAAAAAAGAAAAAAGAAAAAAGAAAAA 1877
Db 1684 AAAAAAAGAAAAAAGAAAAAAGAAAAA 1711

RESULT 3

US-08-701-265-3
; Sequence 3, Application US/08701265
; Patent No. 5776457
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,265
FILING DATE: 22-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B

REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

US-08-701-265-3

Query Match 51.9%; Score 974.4; DB 2; Length 1737;
Best Local Similarity 76.1%; Pred. No. 1.2e-181;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;
QY 50 GCAGGTAGCAGTACCCCTCTGAGCGGTTTGGTGCCTCGGTAAACCAACGCGCTGTAGAC 109
Db 20 GCAGCGGCAAGTAGCAGCGCGAGGCGCTGAGTCTCCAGTACGCCAGCGCATCTGGAGAAC 79

QY 110 GAGTGTGGCCATGGAAACCGATCAGTGTGAGTATATACACTTCTGTATAACTACTCTGTAAGA 169
Db 80 CAGCGGTACCATGGA-----GGGGATCAGTATATACACTTTCAGATAACTACACCGAGGA 134
QY 170 AGTGGGGTCTGAGAGACTATGACTCCAAACAGGAAACCTGCTTCCGGGATGAAAAAGTCCA 229
Db 135 AATGGGCTCAGGGGACTATGACTCCATGAAGGAACCTGTTTCCGTGAAGAAAAATGCTAA 194
QY 230 TTTCAATAGGATCTTCCCTGCGCCACCATCTACTTTCATCATCTTCTTGTGACGTGGCATAGTCG 289
Db 195 TTTCAATAAAATCTTCTGCGCCACCATCTACTTCCATCATCTTCTTAACTGGCATGTGGG 254
QY 290 CAATGATTGGTGAATCTCTGCTCATGGGTTACAGAGAAAGCTAAGGAGCATGACGGACAA 349
Db 255 CAATGATTGGTCACTCTCTGCTCATGGGTTACAGAGAAACTGAGAAGCATGACGGACAA 314
QY 350 GTACCGGCTGCAACCTGTGAGTGGCTGACCTCTCTTGTGTCATCACACTCCCTTCTGGGC 409
Db 315 GTACAGGCTGCACCTGTCTAGTGGCGGACCTCTCTTGTGTCTCATCAGCTTCCCTTCTGGGC 374
QY 410 AGTTGATGCCATGGGCTGACTGTCTTTGGGAAATTTTGTGTAGGGCTGTCCATCAT 469
Db 375 AGTTGATGCCGCGGCAACTGTGACTTTTGGGAACTTCTTATGCAAGGCACTCATGTGAT 434
QY 470 CTACACTGTCAAACCTCTACAGCAGCGGTTCTCATCTGGGCTTTCATCAGCTCGACCGGTA 529
Db 435 CTACACAGTCAACCTCTACAGCAGTGTCTCTCATCTGGGCTTTCATCAGTCTGGACGCTA 494
QY 530 CTTGCGCATTTGCCAGCCCAACAGTCAAAAGGCCAAGGAACTGCTGGCTGAAAAGGC 589
Db 495 CTTGCGCATCTGTCAGCCCAACAGTCAAGAGGCCAAGGAACTGTTGGCTGAAAAGGT 554
QY 590 AGTCTATGTGGGCGTCTGGATCCAGCCCTCTCTGACTATACCTGACTTTCATCTTTGC 649
Db 555 GGTCTATGTGGGCTCTGGATCCCTGCGCTCTCTGCTGACTATTCGCGATTTCTATCTTGC 614
QY 650 CGACGTTCAGCCAGGGGGAATCAGTCAGGGGGATGACAGGTACATCTGTGACCGCTTTA 709
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QY 710 CCCCAGATACCTGTGGATGGTGGTGTTCATTCAGCATATATAAGTGGTGGTCTCATCT 769
Db 660 CCCCAGATACCTGTGGTGGTGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 719
QY 770 GCGCGCATCTGCTCTCTCTGTTTACTGTCATCATCTCTTAAGTCTGTACACTCCAA 829
Db 720 GCTGTGATTTGTCATCTCTCTCTCTGTTTGTGCAATATCATCTCAAGCTGTACACTCCA 779
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Db 780 GGGCCACCAAGAGCGCAAGGCCCTCAAGACCAAGTCACTCTCATCTGGCTTTCTTGC 839
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Db 840 CTGTTGGCTGCTTACTACATTTGGGATCAGCATCGACTCTCTTCATCTCTCTGGAATCAT 899
QY 950 CAGCAAGCATGTGACTTCAGAGCATTTCTGCACAAAGTGCATCTCCATCAGAGAGCCCT 1009
Db 900 CAGCAAGGGTGTGAGTTTGAGAACTGTGTGCAAAAGTGGATTTTCATCAGCGAGGCCCT 959
QY 1010 CGCTTTCTTCCACTGTGTGCTGAACCCCATCTCTATGCTTCTCTGGGGCCAAAGTTCAA 1069
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QY 1130 CAAAGGAAAGCGGGTGGACACTCTTCTCGCTCCAGGAGTCAAGATCTCTCAGATTTTCA 1189
Db 1080 CAAAGGAAAGCGGGTGGACATTCATCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTCA 1139
QY 1190 CTCAGCTAACCCCTTATGCAAGACTTATATATATATATATATATATATATATATATAT 1249

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Db 1140 CTCAGCTAA-----CACAGATGTAAGAGCTTTTATACGATAAATACTTTT 1191
Qy 1250 TTTTATGTTACACATTTTCCAGATATAAGAGACTGACCACTCTGTACAGTTTTTTTTT 1309
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Qy 1310 TTTTAAATGACTGTTGGGAGTTTATGTTCTCTAGTTTTTTTGTGAGGTTTGACTTAATTT 1369
Db 1252 TTGTTGGAATTTTGT-----CTTGTGTTTCTTTAGTATTTTGTGAAGTTAAATGACTTA 1305
Qy 1370 ATATAAATATTTTGTGTTTGTGTTTCTCATGATGAGCTGTAGGAGCACTGTGGCC 1429
Db 1306 TTTATA-----TAAATTTTTTGTGTTTCTCATGATGAGCTGTAGGAGCACTGTGGCC 1361
Qy 1430 AAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGAGCTGTAGAACTGTAGAGGAAGAACTGA 1489
Db 1362 AAGTTCTTAGTGTCTGTCTGCTGTAGGAGCTGTAGAA-----AAGGGAAGCTGA 1413
Qy 1490 ACATTCAGAAATGTGTGTTAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1549
Db 1414 ACATTCAGAGCGGTAGTGAATCAGCTGAAATGAAATGAAATGAAATGAAATGAAATGAA 1473
Qy 1550 TAATCTCTTCAATCCGAGGAGCACCACCCACCCACCCACCCACCCACCCACCCATCTTAA 1609
Db 1474 TAGATAATCTCTCA-----1488
Qy 1610 TGTGTTGTTATGCTGTGTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1669
Db 1489 -----TTCCGTTGGAACGTTTTCCTGTTCTTAAGACGTGAT 1525
Qy 1670 TTTTCTGTAAGAGATGCACTTAAACCAAGCTGAAATGTTGTTGTTGTTGTTGTTGTTG 1729
Db 1526 TTTGCTGTAGAGATGCACTTAAACCAAGCTGAAATGTTGTTGTTGTTGTTGTTGTTGTT 1581
Qy 1730 TTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1789
Db 1582 -----TTTTTCAGTTTTCAGGAGTGGGTTGATTTTCAGCACCTTAC-AGT 1623
Qy 1790 GTACAGCTTTGTTATGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTT 1849
Db 1624 GTACAGCTTTGTTATGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTT 1683
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RESULT 4

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US-08-284-586-3
; Sequence 3, Application US/08284586
; Patent No. 5840856
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,586

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; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 nucleotides
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-284-586-3

Query Match 51.9%; Score 974.4; DB 2; Length 1737;
Best Local Similarity 76.1%; Pred. No. 1.2e-181;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

Qy 50 GCAGGTAGCAGTGCACCTCTGAGGCGTTTGGTGCTCGGTAAACCAACGCGCTGTAGAGC 109
Db 20 GCAGGCGCAAGTGAAGCGGAGGCGCTGAGTGCTCCAGTAGCCACCGCATCTGGAGAAC 79
Qy 110 GAGTGTGGCCATGCAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTCTGAAGA 169
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Qy 170 AGTGGGGCTGTGAGAGACTATGACTCCAAAGAAAGCCCTGCTCCGGGATGAAACGTTCA 229
Db 135 AATGGGCTCAGGGGACTATGACTCCATGAAGAAACCTGTTCCGTGAAGAAATGCTAA 194
Qy 230 TTTCAATAGGATCTTCTGCGGACCACTACTTTCATCATCTTCTTGCATGCGCATAGTCGG 289
Db 195 TTTCAATAAATCTTCTGCGGACCACTACTTTCATCATCTTCTTAACTGGCATTTGTGG 254
Qy 290 CAATGATGTTGTCATCTGTCATGCTTACCAAGAAAGCTTAAGAGCATGACGGACAA 349
Db 255 CAATGATGTTGTCATCTGTCATGCTTACCAAGAAAGCTTAAGAGCATGACGGACAA 314
Qy 350 GTACCGGCTGCACCTGTCTAGTGGCTGACCTCTCTTTTGTGCATCACACTCCCTTCTGGGC 409
Db 315 GTACAGGCTGCACCTGTCTAGTGGCGGACCTCTCTTTTGTGCATCACACTCCCTTCTGGGC 374
Qy 410 AGTTGATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 469
Db 375 AGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
Qy 470 CTACACTGTCACCTCTACAGCAGCTTCTCATCTGCGGCTTCTCATGAGCTGACCGGTA 529
Db 435 CTACAGCTCAACCTCTACAGCAGCTTCTCATCTGCGGCTTCTCATGAGCTGACCGGTA 494
Qy 530 CTTGCGCATTTGTCAGCGCCACCAAGCTCAAGGCGCAAGGAACTGTGTGGCTGAAAGGC 589
Db 495 CTTGCGCATTTGTCAGCGCCACCAAGCTCAAGGCGCAAGGAACTGTGTGGCTGAAAGGC 554
Qy 590 AGTTATGTTGGGCTGTGATCCAGCGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 649
Db 555 GGTCTATGTTGGGCTGTGATCCAGCGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
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/ APPLICATION NUMBER: 08/076093
/ FILING DATE: 11-JUN-1993
/ PRIOR APPLICATION DATA: 07/810782
/ APPLICATION NUMBER:
/ FILING DATE: 19-DEC-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P0706P2P1D2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-5530
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1737 base pairs
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Single
/ TOPOLOGY: Linear
/ US-08-802-627A-3

Query Match 51.9%; Score 974.4; DB 2; Length 1737;
Best Local Similarity 76.1%; Pred. No. 1.2e-181;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;
QY 50 GCAGGTAGCAGTGCACCTCTGAGCGCTTTGGTCTCCGGTAAACCACCGGCTGTAGAGC 109
Db 20 GCGCGGCGCAAGTGAAGCGGAGGCGCTGAGTGCTCCAGTAGCACCGGATCTGGAGAAC 79
QY 110 GAGTGTGGCATGGAACCGCATCAGTGTGAGTATATACATCTTCGTAAACTACTCTGAAGA 169
Db 80 CAGCGGTACCATGGA-----GGGGATCAGTATATACATCTCAGATAACTACACCGGGA 134
QY 170 AGTGGGGTCTGGAGACTATGACTCCAAACAGGAACCGTCTCCGGGATGAAGAACGTCCA 229
Db 135 AATGGGCTCAGGGGACTATGACTCCATGAGGAACCGCTGTTCCGTGAAGAAAATGCTAA 194
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QY 350 GTACCGGCTGCACCTGTGTCAGTGTGACCTCTCTTTGTGTCATCAGTCCCTCTTGGGC 409
Db 315 GTACAGGCTGCACCTGTGTCAGTGTGCGACCTCTCTTTGTGTCATCAGCGCTTCCCTTCTGGGC 374
QY 410 AGTTGATGCCATGGCTGACTGTGTTGTTGGGAAATTTTGTGTAAGGCTGTCCATATCAT 469
Db 375 AGTTGATGCCGTGGGAAATCTGGTACTTTTGGGAACTTCTTATGCAAGGAGTCCATGTAT 434
QY 470 CTACACTGTCAACTCTCTACAGCAGCGTTCTCATCTGGCCCTTCATCAGCCTGGACCGGTA 529
Db 435 CTACACAGTCAACTCTACAGCAGTGTCTCTCATCTGGCCCTTCATCAGTCTGGACCGCTA 494
QY 530 CTTGCGCATTTGTCAGGCCAACCAAGTCAAGGCCAAGGAACTGTGCTGGCTGAAAGGC 589
Db 495 CTTGCGCATCTGTCAGGCCAACCAAGTCAAGGCCAAGGAACTGTGCTGGCTGAAAGGT 554
QY 590 AGTCTATGTGGGCTGTGGATCCAGCCCTCTCTGACTATACCTGACTTTCATCTTTGTC 649
Db 555 GGTCTATGTGGGCTGTGGATCCCTGCGCTCTCTGCTGACTATTTCCGACTTTCATCTTTGC 614
QY 650 CGACGTCAGCGAGGGGACATCAGTCAAGGGGATGACAGGTATACCTGTGACCGCCCTTTA 709
Db 615 CAAAG-----TCAGTGAAGCAGATGACAGATATATCTGTGACCGCTTCTA 659
QY 710 CCCCAGTAGGCTGTGGATGGTGTGTTTCAATTCAGCATATATATGGTGGGCTCATCCT 769
Db 660 CCCCAATGACTTGTGGGTGGTGTGTTCCAGGTTTCAGCATCATGTGGTGGCTTATCCT 719

QY 770 GCCCGCATCGTCATCTCTCTGTTACTGTCATCATCTCTTAAGCTGTCACTCCAA 829
Db 720 GCCTGGTATTGTCACTCTCTCTGCTATTGCAATATCATCTCAAGCTGTCACTCCAA 779
QY 830 GGGCCACCAAGAGCGCAAGGCCCTCAAGACGAGTCATCTCTAGCTTTCTTTGC 889
Db 780 GGGCCACCAAGAGCGCAAGGCCCTCAAGACCAAGTCATCTCTAGCTTTCTTTGC 839
QY 890 CTGCTGGCTGCCATATATTGCGGATCAGCATCGACTCTCTTCATCTTTTGGAGTCAT 949
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QY 950 CAAGCAAGGATGTGACTTCGAGAGCATTTGTGCAAGTGGATCTCCATCAGAGAGCCCT 1009
Db 900 CAAGCAAGGATGTGAGTTTGAGAACACTGTGCAAGTGGATTTCCATCAGCGAGGCCCT 959
QY 1010 CGCCTTTCTTCCATCTGTTGCTGAAACCCCATCTCTATGCTCTCTTGGAGCCAAATTTAA 1069
Db 960 AGCTTTCTTCCATCTGTTGCTGAAACCCCATCTCTATGCTCTCTTGGAGCCAAATTTAA 1019
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Db 1020 AACTCTGCCAGCAGCACTCACTCTCTGAGCAGAGGCTCCAGCTCAAGATCTCTCTC 1079
QY 1130 CAAAGAAAAGCGGGGTGGACACTCTTTCCGTCTCCACGAGTCAGATCTCTCCAGTTTCA 1189
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QY 1370 ATATAAATATGTTTGTGTTTGTTCATGTGAATGAGGCTTAGCAGGACCTGTGGCC 1429
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QY 1430 AAGTCTTAGTGTAGTCTTTATCTGTGTAGGACTCTAGAACTGTAGAGGAAGAACTGA 1489
Db 1362 AAGTCTTAGTGTGTGTATGTCTGCTGGTAGACTGTAGAA-----AAGGGAAGTGA 1413
QY 1490 ACATTCAGAAATGTGTGTTAAATTTGAATAAAGCTAGCCGTGATCTCTCAGCTGTGTGCA 1549
Db 1414 ACATTCAGAGCGGTGTAGTGAATCAGTAAAGCTAGAAATGATCCCGAGCTGTTATGCA 1473
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Db 1474 TAGATAATCTCTCCA-----TTCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1488
QY 1610 TGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1669
Db 1489 -----TTCCTGTTGAAACGTTTTCCTGTTCTTAAGACGTGAT 1525
QY 1670 TTTTCTGTAAGAGATGGCACCTTAAACCAAGCCCTGAAATGGTGGTAGAAATGCTCGGGT 1729
Db 1526 TTTGCTGTAGAGATGGCACCTTATACCAAGCCCAAGTGTGTTATAGAAAATGCTGG--- 1581
QY 1730 TTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1789
Db 1582 -----TTTTTCAGTGTTCAGGAGTGGGTTGATTTTTCAGCACCCTAC-AGT 1623
QY 1790 GTACAGTCTTGTATTACATTTGTTTAAATAAGTCAATGATAAACTTAAATAAAAAA 1849
Db 1624 GTACAGTCTTGTATTAAAGTTGTTTAAATAAGTACATGTTAAACTTAAATAAAAAA 1683
QY 1850 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1877

SEQUENCE CHARACTERISTICS:

LENGTH: 1737 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

PCT-US94-06380-2

Query Match 51.9%; Score 974.4; DB 6; Length 1737;

Query Match
Best Local Similarity
76.1%; Pred. No. 1.2e-181;
31.5%; score 974.4; DB 6

Seq. ID	Seq. Name	Seq. Length	Seq. Type	Seq. Source	Seq. Accession	Seq. Date	Seq. Status	Seq. Notes
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2	Seq. 2	100	Protein	Human	Q12346	2023-10-27	Complete	Initial sequence
3	Seq. 3	100	Protein	Human	Q12347	2023-10-27	Complete	Initial sequence
4	Seq. 4	100	Protein	Human	Q12348	2023-10-27	Complete	Initial sequence
5	Seq. 5	100	Protein	Human	Q12349	2023-10-27	Complete	Initial sequence
6	Seq. 6	100	Protein	Human	Q12350	2023-10-27	Complete	Initial sequence
7	Seq. 7	100	Protein	Human	Q12351	2023-10-27	Complete	Initial sequence
8	Seq. 8	100	Protein	Human	Q12352	2023-10-27	Complete	Initial sequence
9	Seq. 9	100	Protein	Human	Q12353	2023-10-27	Complete	Initial sequence
10	Seq. 10	100	Protein	Human	Q12354	2023-10-27	Complete	Initial sequence
11	Seq. 11	100	Protein	Human	Q12355	2023-10-27	Complete	Initial sequence
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19	Seq. 19	100	Protein	Human	Q12363	2023-10-27	Complete	Initial sequence
20	Seq. 20	100	Protein	Human	Q12364	2023-10-27	Complete	Initial sequence
21	Seq. 21	100	Protein	Human	Q12365	2023-10-27	Complete	Initial sequence
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24	Seq. 24	100	Protein	Human	Q12368	2023-10-27	Complete	Initial sequence
25	Seq. 25	100	Protein	Human	Q12369	2023-10-27	Complete	Initial sequence
26	Seq. 26	100	Protein	Human	Q12370	2023-10-27	Complete	Initial sequence
27	Seq. 27	100	Protein	Human	Q12371	2023-10-27	Complete	Initial sequence
28	Seq. 28	100	Protein	Human	Q12372	2023-10-27	Complete	Initial sequence
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31	Seq. 31	100	Protein	Human	Q12375	2023-10-27	Complete	Initial sequence
32	Seq. 32	100	Protein	Human	Q12376	2023-10-27	Complete	Initial sequence
33	Seq. 33	100	Protein	Human	Q12377	2023-10-27	Complete	Initial sequence
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38	Seq. 38	100	Protein	Human	Q12382	2023-10-27	Complete	Initial sequence
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110	GAGTGTTCGCCATGGAAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTCTGAAGA	169
80	CAGCGGTTACCATGGAA-----GGGGATCAGTATATACACTTTCAGATAACTACACCGAGGA	134
170	AGTGGGGTCTGGAGAGCTATGACTCCAAACAGGAACCCCTGCTCCGGGATCAAAACGTCCTCA	229
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255	CAATGGGAATTGGTCATCCTGTGTCAATGGTTTACCAAGAAAGAACTGAGAAGCATGACGACAA	314
350	GTACCGGCTGCACCTGTCTAGTGTGCTGACCTCTCTTTGTGCATCACACTCCCTTCTGGGC	409
315	GTACAGGCTGCACCTGTCTAGTGTGCGGACCTCTCTTTGTCTCATCAGCGTTCCCTTCTGGGC	374
410	AGTTGATGCCATGGCTGCACTGGTACTTTTGGGAAATTTTGTGTAAAGCTGTCCATATCAT	469
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470	CTACACTGTCAACCTCTACAGCAGGTTTCTATCTCTGGCCCTTTCATCAGCTGTGACCGGTA	529
435	CTACACAGTCAACCTCTACAGCAGTGTCTCATCTCTGGCCCTTTCATCAGTCTGGACCGCTA	494
530	CCTCGGCATTTGTCCAGCCACCAACAGTCAAAAGGCCAAGGAAACTGCTGCTGAAAGGC	589
495	CCTGGCCATCTGTCCAGCCCAACCAAGTCAAGAGGCCAAGGAGCTGTGGCTGAAAGGT	554
590	AGTCTATGTGGGGTCTGGATCCAGCCCTCTCTCTGACTATATCCTGACTTCATCTTTGC	649
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650	CGACGTCAGCCAGGGGGACATCAGTCAGGGGGATGACAGGTACATCTGTGACCGCCCTTTA	709
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770	GGCCGCGCATCGTCATCCTCTCTGTTTACTGTCATCATCTCTTAAGTGTTCACACTCCAA	829
720	GGCTGGTATTGTTCATCCTGTCTGTGCTATTGTCATTATCATCTCCAAGCTGTTCACACTCAA	779
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780	GGGCCACCAAGAGCGCAAGGCCCTCAAGACCAAGTCACTCCTCATCTCTGCTTTCTTCGC	839
890	CTGCTGGCTGCCATAATTATGTGGGGATCAGCATCGACTCCTTTCATCTTTTGGGAGTCAT	949
840	CTGTGGCTGCCTTACTACATTGGGATCAGCATCGACTCTTTCATCTCTCTCGGAATCAT	899
950	CAAGCAAGGATGTGACTTTGGAGAGCAATTGTGCAAAAGTGGATCTCCATCAACAGAGCCCT	1009

; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-517-605-14

Query Match 50.8%; Score 952.8; DB 3; Length 1679;
Best Local Similarity 80.2%; Pred. No. 2.1e-177;
Matches 1210; Conservative 0; Mismatches 252; Indels 46; Gaps 6;

QY 44 GCAGGTGCGAGGTAGCAGTACCCCTCTGAGCGGTTTGGTCTCGCGGTAAACCACACCGCTG 103
DB 12 GCGGCAGCAGGTAGCAAGTGACGCGGAGGGCTGAGTGTCTCCAGTAGCCACCGCATCTG 71
QY 104 TAGAGGAGTGTGCCATGGAACCGATCAGTGTGAGTATATACATCTCTGATTAACCTACTC 163
DB 72 GGAACACAGCGGTATACATGGA-----GGGGATCAGTATATACATCTCAGATAACTACAC 126
QY 164 TGAAGAAGTGGGCTCTGGAGACTATGACTCCAAAGGAACCCCTGCTTCGGGATGAAGA 223
DB 127 CGAGGAATAGGGCTCAGGGGACTATGACTCCATGAAGGAACCCGTTTCCGTGAAGAAA 186
QY 224 CGTCCATTTCAATPAGGATCTTCCTGCCACCATCTACTTTCATCATCTCTTTGATGGCAT 283
DB 187 TGTCTAATTTCAATAAATCTTCCTGCCACCATCTACTTTCATCATCTCTTTAACTGGCAT 246
QY 284 AGTCGGCAATGGATTGGTGTATCTGTGTCATGGTTTACCAGAAAGCTTAAGGAGCATGAC 343
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QY 344 GGACAGTACCGGCTGCACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 403
DB 307 GGACAGTACCGGCTGCACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 366
QY 404 CTGGGCGAGTTGATGCCATGGCTGACTGGTATCTTTGGGAAATTTTGTGAAGCTGTCCA 463
DB 367 CTGGGCGAGTTGATGCCATGGCTGACTGGTATCTTTGGGAAATTTTGTGAAGCTGTCCA 426
QY 464 TATCATCTACATCTGTAACCTCTACAGCAGCGTTCTCATCTGGCCTTCTATCAGCCTGGA 523
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QY 524 CCGGTACCTCGCCATGTGTCCAGCCCAACACAGTCAAGGCCCAAGGAACTGTGGCTGA 583
DB 487 CCCTTACCTGGCCATGTGTCCAGCCCAACACAGTCAAGGCCCAAGGAACTGTGGCTGA 546
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QY 644 CTTTGGCGAGCTCAGCAGGGGAGACATCAGTCAAGGGGATGACAGGTATCTGTGACCG 703
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DB 652 CTTTACCCCAATGACTTTGTGGGTGTGTTTCCAGTTTTCAGCATATATGTGGGTCT 711
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DB 712 TATCTCTCGCTGGTATTGTCTATCTCTCTCTGTTTACTGATCATCATCTCTCAAGCTGTGACA 771
QY 824 CTCACAGGGCCACAGAGGGCCAGGGCCCTCAAGCAGCAGTATCTCTCATCTCTAGCTTT 883
DB 772 CTCACAGGGCCACAGAGGGCCAGGGCCCTCAAGCAGCAGTATCTCTCATCTCTAGCTTT 831
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DB 832 CTTGCGCTGTGGCTGCTTACTACATTGGGATCAGCATCGACTCTTTCATCTCTCTGGA 891
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QY 1184 TTTTCACTCCAGTAACTTATGCAAGACTTATATATATATATATATATATATATATATAA 1243
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QY 1304 TTTTATTTTAAATGACTGTGGGAGTTTATGTTCTCTAGTTTGTGAGGTTTGACT 1363
DB 1244 TATGCTTGTGGATTTTGT-----CTTGTGTTTCTTTAGTTTGTGAAAGTTTAAAT 1297
QY 1364 TAATTATATATAATTTGTTTGTGTTTTCATGTGAATGAGCTCTAGGCAGGACCT 1423
DB 1298 GACTTATTTATA-----TAAATTTTGTGTTTTCATATGATGTGTCTAGGCAGGACCT 1353
QY 1424 GTGGCCAACTTCTTAGTACTGTATCTGTGTAGGACTGTAGAACTGTAGAGGAAGA 1483
DB 1354 GTGGCCAACTTCTTAGTCTGTATGTCTGTGTAGGACTGTAGAA-----AAGGG 1405
QY 1484 AACTGAACATTCAGAAATGTGGTAAATGAAATGAATGAATGAATGAATGAATGAATGA 1543
DB 1406 AACTGAACATTCAGAGAGCTGTAGTGAATCAGGTAAAGCTAGAAATGATCCCAGCTGT 1465
QY 1544 GCTGCATA 1551
DB 1466 TATGCATA 1473

RESULT 12
US-09-582-224A-5
; Sequence 5, Application US/09582224A
; Patent No. 6429308
; GENERAL INFORMATION:
; APPLICANT: IJIMA, Osamu
; APPLICANT: GOTO, Takeshi
; APPLICANT: SHIMADA, Takeshi
; TITLE OF INVENTION: HIV Infection Inhibitors
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/582,224A
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: PCT/JP99/06534
; PRIOR FILING DATE: 1999/11/24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1664
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA of CXCR4
US-09-582-224A-5

Query Match 50.7%; Score 951.8; DB 3; Length 1664;

1001	TTTTAAACTCTGCCCGACGACCTCACTCTGTGAGCAGAGGGTCCAGCCTCAAGATC	1061
1125	CTTTCCAAAGAAAGCGGGTGGACACTCTTCGGTCTCCACGGAGTCAGAAATCCTCCAGT	1184
1061	CTCTCCAAAGAAAGCGAGGTGGACATTCATCTGTTTCCACTGAGTCTGAGTCTTCAAGT	1120
1185	TTTCACTCCAGCTAACCCCTTATGCAAGACTTATATAAATATATATATATATATATATGATAAG	1244
1121	TTTCACTCCAGCTAACACAGATGTAAAGACTTTTTT-----TTTATACGATAAATA	1172
1245	AACCTTTTATGTTACACATTTTCCAGATATATAAGACACTGACCAGTCTGTACAGTTTTT	1304
1173	CTTTTATTAAGTTACACATTTTTCAGATATAAAGACTGACCAATATTGTACAGTTTTT	1332
1305	TTTTTTTTTAATGACTGTGGGAGCTTATGTTCTCTAGTTTTTGTGAGGTTTGCACCT	1364
1233	ATTGCTTGTGGATTTTCT-----CTTGTGTTCTTTAGTTTTTGTGAAGTTTAATTG	1286
1365	AATTTATATAATATGTTTTTTTGTGTTTTCATGTAATGAGCGTCTAGGCAGGACCTG	1424
1287	ACTTATTTATA---TAAATTTTTTTTGTTCATATGATGTGTCTAGGCAGGACCTG	1342
1425	TGGCCAAGTCTTAGTAGCTGTTTATCTGCTGTGAGGACTGTAGAACTGTAGAGGAAGAA	1484
1343	TGGCCAAGTCTTAGTGTCTGTATGTCCTGCTGAGGACTGTAGAA-----AAGGGA	1394
1485	ACTGAACATTCAGAAATGTGTGTAATGAATAAAGCTAGCCGTCATCTCAGCTGTTG	1544
1395	ACTGAACATTCAGAGCGTGTAGTTAATCAGCTAAAGCTAGAAATGATCCCAGCTGTTT	1454
1545	CTGCATA 1551	
1455	ATGCATA 1461	

RESULT 13

US-09-023-655-1213

; Sequence 1213, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESS: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0001 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

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; INFORMATION FOR SEQ ID NO: 1213:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1664 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g219868
; US-09-023-655-1213

Query Match      50.7%; Score 951.8; DB 3; Length 1664;
Best Local Similarity 80.2%; Pred. No. 3.3e-177;
Matches 1209; Conservative 0; Mismatches 252; Indels 46; Gaps 6;

QY 45 CAGGTGAGTAGCAGTACGACCTCTGAGGCGTTTGGTGTCCGGTAAACCAACACGGGTGT 104
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QY 105 AGAGCAGGTGTTGCCATGGNAACGATCAGTGTGAGTATATACACTTCTGATTAAGTACTCT 164
Db 61 AGAACAGCGGTTTACCATGGA-----GGGGATCAGTATATACACTTTCAGATAACTACACC 115
QY 165 GAAGAAATGGGTCTGGAGACTATGACTCCAAAGGAACCCCTGCTTCCGGGATGAAAC 224
Db 116 GAGGAATGGGTCTCAGGGACTATGACTCCATGAGGAACCCCTGTTCCGTGAAGAAAT 175
QY 225 GTCATTTCAATAGGATCTTCCGCGCCACCATCTACTTCATCATCTTCTTGAATGGGATA 284
Db 176 GCTAAATTTCAATAAAATCTTCTGCGCCACCATCTACTCCATCATCTTCTTAACTGGCAIT 235
QY 285 GTCGGCAATGGATGTGTGATCTCTGTCATGCTGATGCTTACGAGGAAGCTTACGAGCATGACG 344
Db 236 GTGGGCAATGGATGTGTGATCTCTGTCATGCTGCTGCTTACGAGGAACCTGAGAGCATGACG 295
QY 345 GACAAGTACCGGCTGCACCTGTGAGTGGCTGACCTCTCTTTGTGTCATCACACTCCCTTTC 404
Db 296 GACAAGTACAGGCTGCACCTGTGAGTGGCGGACCTCTCTTGTGTCATCAGCTTCCCTTC 355
QY 405 TGGGAGTTGATGCGCATGGCTGATCTGTGATCTTTGGGAAATTTTGTGTGAAGCTGTCCAT 464
Db 356 TGGGAGTTGATGCGCTGGCAAACTGTGATCTTTGGGAACTTCTATGCAAGGCGAGTCCAT 415
QY 465 ATCATCTACACTGTCAACCTCTACAGCAGGCTTCTCATCTGCGCTTTCATCAGCCTGGAC 524
Db 416 GTCATCTACAGTCAACCTCTACAGCAGTGTCTCATCTGCGCTTTCATCAGTCTGGAC 475
QY 525 CGGTACTCTCGCCATTTGCCAGCCACCAACAGTCAAAGGCCAAGGAACTGTGGCTGAA 584
Db 476 CGCTACTTGGCCATCTGCCAGCCACCAACAGTCAAGGCCAAGGAACTGTGGCTGAA 535
QY 585 AAGGAGTCTATGTGGGCTGTGGATCCAGCCCTCTCTGACTATATCTGACTTCACTCATC 644
Db 536 AAGTGTGTATGTGGGCTGTGGATCCAGCCCTCTCTGACTATATCTGACTTATCCCGACTTCATC 595
QY 645 TTTGCGAGCTCAGCCAGGCGGACATCAGTCAGGGGATGACAGGTACATCTGTGACCGC 704
Db 596 TTTGCCAACG-----TCAGTGGGAGATGACAGATATATCTGTGACCGC 640
QY 705 CTTTACCCCGATGCTGTGGATGGTGTGTTTCAATTCAGCATATAATGTGGGTCTC 764
Db 641 TTTCAACCCCAATGACTTGTGGGTGGTGTGTTCCAGTTTCAGCACATCATGTTGGCTT 700
QY 765 ATCTGCGCGGATGCTGATCTCTCTCTGTTACTGTGATCATCTATCTTAAGCTGTACAC 824
Db 701 ATCTGCTGCTGTTATGTGATCTCTCTCTCTGTTATTTGATATATCATCTCCAAAGCTGTACAC 760
QY 825 TCCAAGGCCACCAAGAGCCCAAGGCCCTCAAGACGACGTATCTCATCTCACTGCTTTC 884
Db 761 TCCAAGGCCACCAAGAGCCCAAGGCCCTCAAGACGACGTATCTCATCTCTGCTTTC 820
QY 885 TTTGCTGCTGCTGCTGCTATATATGTGGGATCAGCATCGACTCTCTCATCTCTTTGGGA 944
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Db 821 TTGCGCTGTGTGCTGCTTACTACATTTGGGATCAGCATCGACTCTCTTCATCTCTCTGGAA 880
QY 945 GTCATCAAGCAAGGATGTGACTTCGAGAGCATTTGTCACAAGTGGATCTCCATCACAGAG 1004
Db 881 ATCATCAAGCAAGGATGTGAGTTGAGAACACTGTGCAACAGTGGATTTCCATCACCGAG 940
QY 1005 GCCTCGCTTCTTCCACTGTGTGCTGAAACCCCATCTCTATGCGCTTCTCTCGGGGCCAAG 1064
Db 941 GCCTAGCTTCTTCCACTGTGTGCTGAAACCCCATCTCTATGCTTCTCTCGAGGCCAA 1000
QY 1065 TTCAAAGCTCTGCCAGCATCACTCAACTCAATGAGCAGAGGCTCCAGCTCAAGATC 1124
Db 1001 TTTAAACCTCTGCCAGCAGCAGCTCACTCTGTGAGCAGAGGCTCCAGCTCAAGATC 1060
QY 1125 CTTTCCAAAGGAAGCGGGGTGAGCACTCTTCGCTCCACGAGTCAAGATCTCCAGT 1184
Db 1061 CTCTCCAAAGGAAGCGGGGTGAGCACTTCATCTGTTTCCACTGAGTCTGAGTCTTCAAGT 1120
QY 1185 TTTCACTCCAGCTAACCCCTTATGCAAGACTTATATAATATATATATATATATATATAAAG 1244
Db 1121 TTTCACTCCAGCTAACAGATGTAAGACTTTTT-----TTTATACGATAATAA 1172
QY 1245 AACTTTTTTATGTACACATTTTCCAGATATAAGAGACTGACAGTCTTGTACAGTTTTT 1304
Db 1173 CTTTTTTTTAAGTTACACATTTTTCAGATATAAAGACTGACCAATATTTGTACAGTTTTT 1232
QY 1305 TTTTTTTTTAATTGACTGTGCGGAGTTTATGTTCTCTAGTTTTTTGTGAGGTTTGCATT 1364
Db 1233 ATTGCTGTGTGAGTTTTTGT-----CTTGTGTCTTCTTGTGAGGTTTAAATTG 1286
QY 1365 AATTATATAAATATTTTGTGTTTTCATGTGAATGAGCGTCTAGGCGAGGACCTG 1424
Db 1287 ACTTATTATA-----TAAATTTTTTTTGTTCATATTGATGTGTCTAGGCGAGGACCTG 1342
QY 1425 TGGCAAGTCTTAGTAGCTGTTTATCTGTGTGAGGACTGTAGAACTGTAGAGGAAGAA 1484
Db 1343 TGGCAAGTCTTAGTGTCTGTATGCTGCTGCTGAGTGTAGAA-----AAGGGA 1394
QY 1485 ACTGACATTCAGATGTGTGTAATGTAATGTAAGCTAGCGTATCTCAGCTGTTG 1544
Db 1395 ACTGAACATTCAGAGCGGTGTAGTTAATCAGTAAAGCTAGAAATATATCCCGAGCTGTTT 1454
QY 1545 CTGCATA 1551
Db 1455 ATGCATA 1461
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RESULT 14
US-09-016-434-1235
; Sequence 1235, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
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TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 201..1211
US-08-153-848-45

Query Match 44.5%; Score 834.6; DB 2; Length 1317;
Best Local Similarity 83.9%; Pred. No. 2.9e-154;
Matches 977; Conservative 0; Mismatches 164; Indels 24; Gaps 2;

QY	134	TGTGAGTATATACACTTCTGATAACTACTCTGAAGAGTGGGCTCTGGAGACTATGACTC	193
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QY	194	CAAAAGGAACCTGCTTCGCGGATGAACCGTCCATTTCAATAGGATCTTCTGCCCCAC	253
DB	224	CATGAAGGAACCTGTTTCGTGAAGAAATGCTAATTTCAATAAATCTTCTGCCCCAC	283
QY	254	CATCTACTTCATCATCTTCTTGATGCGCATAGTCGGCAATGGATTTGGTGTATCTCTGTCAT	313
DB	284	CATCTACTTCATCATCTTCTTAACTGGCAATGTGGCAATGGATTTGGTCACTCTCTGTCAT	343
QY	314	GGGTTACCAAGAACGTAAGGAGCATGACGGAAGTACCGGCTGCACCTGTCAGTGGC	373
DB	344	GGGTTACCAAGAACGTAAGGAGCATGACGGAAGTACCGGCTGCACCTGTCAGTGGC	403
QY	374	TGACCTCTCTTGTGTCATCACACTCCCTCTCTGGCAGTTGATGCCATGGCTGACTGGTA	433
DB	404	CGACCTCTCTTGTGTCATCACACTCCCTCTCTGGCAGTTGATGCCATGGTGGTA	463
QY	434	CTTTGGGAAATTTTGTGTAAGGCTGTCCATATCATCTACATGTCTCACTCTACAGCAG	493
DB	464	CTTTGGGAAATTTCTTATGCAAGGAGTCCATGTCTATCTACAGTCAACCTCTACAGCAG	523
QY	494	CGTTCTCATCTCGGCTTCATCAGCTGAGCCGCTACCTCGCATTTGTCACCGCCACCA	553
DB	524	TGTCCTCATCTCGGCTTCATCAGCTGAGCCGCTACCTCGCATTTGTCACCGCCACCA	583
QY	554	CAGTCAAAAGGCCAAAGAACTGTGGCTGAAAAGGCAAGTCTATGTGGCGCTCTGGATCCC	613
DB	584	CAGTCAAGAGGCCAAAGAACTGTGGCTGAAAAGGCTCTATGTGGCGCTCTGGATCCC	643
QY	614	AGCCCTCTCTGACTATACCTGACTTCATCTTTGGCGAGCTCAGCCAGGGGGACATCAG	673
DB	644	TGCCCTCTCTGACTATTTCCGACTTTCATCTTTGGCAAGC-----TCAG	688
QY	674	TCAGGGGGATGACAGGTACATCTGTGACCGCTTTACCCCGATAGCTGTGGATGGT	733
DB	689	TGAGGAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGGTGT	748
QY	734	GTTTCAATTCAGCATATAATGGTGGGTCTCATCTGSCCGGCATCGTCACTCTCTCTG	793
DB	749	GTTCAGGTTTCAGCACATCATGTTGGCCCTTATCTCTGCTGGTATTGTCTCTCTGCTG	808
QY	794	TTACTGCATCATCATCTTAAGCTGTACACTCCAGGGGCCACAGAGGCGAAGGCCCT	853
DB	809	CTATTGCATTTATCATCTCCAAAGCTGTACACTCCAGGGGCCACAGAGGCGAAGGCCCT	868
QY	854	CAAGACGACAGTCACTCTCATCTAGCTTTCTTTGGCTGTGGCTGCATATTATGTGGG	913
DB	869	CAAGACGACAGTCACTCTCATCTAGCTTTCTTTGGCTGTGGCTGTGGCTGTGGCTGTGG	928
QY	914	GATCAGCATCGACTCTCTTCATCTCTTTGGGAGTCACTCAAGCAAGGATGTGACTTTCGAGAG	973

DB	929	GATCAGCATCGACTCTCTTCATCTCTCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAA	988
QY	974	CATTGTGCAAGTGGATCTCCATCATCAGAGGCCCTCGCCTTCTTCCACTGTTCCTGAA	1033
DB	989	CACGTGTGCAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTCCACTGTTCCTGAA	1048
QY	1034	CCCCATCTCTATGCTTCTCGGGGCCAAAGTTCAAAAGCTCTGCCCAGCATGCACTCAA	1093
DB	1049	CCCCATCTCTATGCTTCTTGGAGCCAAATTTAAACCTCTGCCCAGCAGCATCTCAC	1108
QY	1094	CTCCATGAGCAGAGGCTCCAGCCTCAAGATCTTTTCCAAAGGAAAGCGGGGTGGACACTC	1153
DB	1109	CTCTGTGAGCAGAGGGTCCAGCCTCAAGATCTCTCCAAAGGAAAGCGAGGTGGACATTC	1168
QY	1154	TTCCGTCTCCAGGAGTCAGAAATCTCCAGTTTTCACCTCCAGTAACTTTTATGTTACACAT	1213
DB	1169	ATCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGCTAACAGATGTAAA--	1226
QY	1214	CTTATATAATATATATATATATATAATAAGAACTTTTATGTTTACACATTTTCCAGAT	1273
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DB	1280	ATAAAAGACTGACCAATATTGAAAA	1304

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)

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Perfect score: 1877

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	93.7	1758	8	US-10-785-230-4
2	974.4	51.9	1737	3	US-09-104-063-3
3	974.4	51.9	1737	7	US-10-666-689-3
4	970	51.7	1826	8	US-10-723-860-5773
5	964.2	51.4	1699	8	US-10-775-920-373
6	960.4	51.2	1662	7	US-10-706-265-11
7	952.8	50.8	1679	5	US-10-151-274-14
8	952.8	50.8	1679	5	US-10-225-567A-75
9	952.8	50.8	1679	6	US-10-021-660-58
10	952.8	50.8	1679	6	US-10-170-385-332
11	952.8	50.8	1679	6	US-10-341-434-177
12	952.8	50.8	1679	6	US-10-172-118-912
13	952.8	50.8	1679	7	US-10-211-462-80
14	952.8	50.8	1679	7	US-10-181-906-9
15	952.8	50.8	1679	7	US-10-342-887-912
16	952.8	50.8	1679	8	US-10-775-920-366
17	952.8	50.8	1679	8	US-10-278-698-64
18	952.8	50.8	1679	8	US-10-278-698-578
19	952.8	50.8	1679	9	US-10-888-313A-62
20	952.8	50.8	1679	9	US-10-486-471-19
21	952.8	50.8	1711	3	US-09-971-392-20
22	952.8	50.8	1711	6	US-10-101-510-459
23	951.8	50.7	1664	7	US-10-641-643-1213

24	951.8	50.7	1664	8	US-10-775-920-369	Sequence 369, App
25	947.6	50.5	1645	8	US-10-775-920-374	Sequence 374, App
26	947.6	50.5	1645	9	US-10-505-680-185	Sequence 185, App
27	944.8	50.3	1670	3	US-09-880-107-2143	Sequence 2143, App
28	944.8	50.3	1670	3	US-09-960-706-636	Sequence 636, App
29	944.8	50.3	1670	6	US-10-372-683-1	Sequence 1, Appli
30	944.8	50.3	1670	7	US-10-440-464-77	Sequence 77, Appli
31	944.8	50.3	1670	7	US-10-717-597-317	Sequence 317, App
32	944.8	50.3	1670	8	US-10-775-920-367	Sequence 367, App
33	938.2	50.3	1950	8	US-10-775-920-368	Sequence 368, App
34	938.2	50.3	1950	8	US-10-723-860-1279	Sequence 1279, App
35	936.8	49.9	1588	8	US-10-785-230-2	Sequence 2, Appli
36	934.4	49.8	5161	6	US-10-160-401-1	Sequence 1, Appli
37	921.2	49.1	1637	8	US-10-775-920-372	Sequence 372, App
38	905.6	48.2	1050	9	US-10-486-706-54	Sequence 54, Appli
39	859	45.8	1225	6	US-10-101-510-741	Sequence 741, App
40	859	45.8	1225	6	US-10-305-720-1235	Sequence 1235, App
41	859	45.8	1225	8	US-10-775-920-370	Sequence 370, App
42	847	45.1	1224	6	US-10-101-510-674	Sequence 674, App
43	809.6	43.1	1059	3	US-09-813-651B-84	Sequence 84, Appli
44	809.6	43.1	1059	6	US-10-014-322A-125	Sequence 125, App
45	809.6	43.1	1059	6	US-10-160-401-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-785-230-4
; Sequence 4, Application US/10785230
; Publication NO. US20040209837A1
; GENERAL INFORMATION:
; APPLICANT: KISHIMOTO, Tadamiu
; APPLICANT: NAGASAWA, Takashi
; APPLICANT: TACHIBANA, Kazunobu
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: Vascularization Inhibitors
; FILE REFERENCE: 46124-5042-US
; CURRENT APPLICATION NUMBER: US/10785,230
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: PCT/JP99/01448
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: JP10/95448
; PRIOR FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Mus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1080)
; OTHER INFORMATION:
US-10-785-230-4
Query Match 93.7%; Score 1758; DB 8; Length 1758;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1758; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 120 ATGGACCCGATCAGTGTGAGTATATACATCTCTGATAAATCTCTCAAGAGTGGGGTCT 179
Db 1 ATGGAAACCCGATCAGTGTGAGTATATACATCTCTGATAAATCTCTCAAGAGTGGGGTCT 60
QY 180 GGAGACTATGACTCCAAACAGGAACCCCTCTCCGGGATGAAACCTCCATTTCAATAGG 239
Db 61 GGAGACTATGACTCCAAACAGGAACCCCTCTCCGGGATGAAACCTCCATTTCAATAGG 120
QY 240 ATCTTCTGCCACCATCTACTTCATCTCTTGAATGGCATAGTCGGCAATGATTG 299
Db 121 ATCTTCTGCCACCATCTACTTCATCTCTTGAATGGCATAGTCGGCAATGATTG 180
QY 300 GTGATCTCTGTCATGGTTTACCAGAGAGTAAAGGAGCATGACGCAAGTACCGGCTG 359

181 GTGATCCTGGTCATGGTTACAGAGAAGCTAAGGAGCATGACGACAAGTAGTACCGGCTG 240
360 CACCTGTGAGTGGCTGACCTCCTTTGTGTATCATCACATCCCTTTCTGGGAGTTGATGCC 419
241 CACCTGTGAGTGGCTGACCTCCTTTGTGTATCATCACATCCCTTTCTGGGAGTTGATGCC 300
420 ATGGCTGACTGGTACTTTGGGAATTTTGTGTAAAGGCTGTGCATATCATCTACACTGTC 479
301 ATGGCTGACTGGTACTTTGGGAATTTTGTGTAAAGGCTGTGCATATCATCTACACTGTC 360
480 AACCTCTACAGACGGTTCTCATCTGGCTTTCATCAGCTGACCGCTGACCGGTACCTGGCAAT 539
361 AACCTCTACAGACGGTTCTCATCTGGCTTTCATCAGCTGACCGGTACCTGGCAAT 420
540 GTCCAGCCACCAACAGTCAAGGCCACAGAACTGCTGCTGAAAGGAGCTATGTG 599
421 GTCCAGCCACCAACAGTCAAGGCCACAGAACTGCTGCTGAAAGGAGCTATGTG 480
600 GGCGTCTGGATCCAGCCCTCCTCTGACTATACCTGACTTCATCTTTGCGGACGTCAGC 659
481 GGCGTCTGGATCCAGCCCTCCTCTGACTATACCTGACTTCATCTTTGCGGACGTCAGC 540
660 CAGGGGACATCATGTCAGGGGATGACAGGTATCATCTGTGACCGCTTTACCCCGATAGC 719
541 CAGGGGACATCATGTCAGGGGATGACAGGTATCATCTGTGACCGCTTTACCCCGATAGC 600
720 CTGTGATGTTGTTGTTTCAATTCAGCATATTAATGGTGGGTCTCATCTGCGCGGATC 779
601 CTGTGATGTTGTTGTTTCAATTCAGCATATTAATGGTGGGTCTCATCTGCGCGGATC 660
780 GTCATCTCTCTCTGTACTGATCATCATCTCTAAGCTGTCACTCCAAAGGGCCACAG 839
661 GTCATCTCTCTCTGTACTGATCATCATCTCTAAGCTGTCACTCCAAAGGGCCACAG 720
840 AAGCGCAAGCCCTCAAGACGACAGTCACTCTCATCTCTAGCTTTCTTTGCTGCTGGCTG 899
721 AAGCGCAAGCCCTCAAGACGACAGTCACTCTCATCTCTAGCTTTCTTTGCTGCTGGCTG 780
900 CCATATATGTTGGGATCAGCATGAGTCTCTCATCTCTTTTGGGAGTCACTCAAGCAAGGA 959
781 CCATATATGTTGGGATCAGCATGAGTCTCTCATCTCTTTTGGGAGTCACTCAAGCAAGGA 840
960 TGTGACTTTCAGAGACATTTGTCACAGTGGATCTCCATCACAGAGCCCTCGCTCTCTTC 1019
841 TGTGACTTTCAGAGACATTTGTCACAGTGGATCTCCATCACAGAGCCCTCGCTCTCTTC 900
1020 CACTGTTGCTGAACCCCATCTCTATGCTTCTCTGGGCGCAAGTTCAAAAGCTCTGCC 1079
901 CACTGTTGCTGAACCCCATCTCTATGCTTCTCTGGGCGCAAGTTCAAAAGCTCTGCC 960
1080 CAGCATGCACTCAACTCCATGACGAGGCTCCAGCTCAAGATCCTTTCCAAAGGAAG 1139
961 CAGCATGCACTCAACTCCATGACGAGGCTCCAGCTCAAGATCCTTTCCAAAGGAAG 1020
1140 CGGGTGGACACTTTCCTCGCTCCAGGAGTCAAGATCTCCAGTTTCACTCCAGCTAA 1199
1021 CGGGTGGACACTTTCCTCGCTCCAGGAGTCAAGATCTCCAGTTTCACTCCAGCTAA 1080
1200 CCCTTATGCAAGACTTATATAATATATATATATATATATATATATATATATATATAT 1259
1081 CCCTTATGCAAGACTTATATAATATATATATATATATATATATATATATATATATAT 1140
1260 CACATTTTCAGATATAGAGACTGACCATCTGTACAGTTTTTTTTTTTTTTTTTAATTG 1319
1141 CACATTTTCAGATATAGAGACTGACCATCTGTACAGTTTTTTTTTTTTTTTTTTTTTAATTG 1200
1320 ACTGTTGGGAGTTTATGTTCTCTAGTTTGTGAGGTTTGACTTAAATTTATATAATAT 1379
1201 ACTGTTGGGAGTTTATGTTCTCTAGTTTGTGAGGTTTGACTTAAATTTATATAATAT 1260
1380 TGTTTTTTGTGTTTTCATGTGAATGAGCGTCTAGGCGAGCCTGTGGCCAAAGTCTTAG 1439
1261 TGTTTTTTGTGTTTTCATGTGAATGAGCGTCTAGGCGAGCCTGTGGCCAAAGTCTTAG 1320

1440 TAGCTGTTTATCTGTGTAGGACTGTAGAACTGTAGAGAAAGAACTGAACATTCAGAA 1499
1321 TAGCTGTTTATCTGTGTAGGACTGTAGAACTGTAGAGAAAGAACTGAACATTCAGAA 1380
1500 ATGTGTGGTAAATTAAGCTAGCCGTGATCCTCAGCTGTGTGCTGCATATCTCTTC 1559
1381 ATGTGTGGTAAATTAAGCTAGCCGTGATCCTCAGCTGTGTGCTGCATATCTCTTC 1440
1560 ATTCCGAGGAGACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCC 1619
1441 ATTCCGAGGAGACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCC 1500
1620 TSCGTGTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1679
1501 TSCGTGTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1560
1680 AAGATGGCACTTAAACCAAAGCTGAAATGGTGGTAAAGTGTCTGGGGTTTTTTTTTGT 1739
1561 AAGATGGCACTTAAACCAAAGCTGAAATGGTGGTAAAGTGTCTGGGGTTTTTTTTTGT 1620
1740 TGTGTTGTTTTCAGTTTCAAGAGTAGATTGACTTCAGTCCCTACAAATGTACAGTCTT 1799
1621 TGTGTTGTTTTCAGTTTCAAGAGTAGATTGACTTCAGTCCCTACAAATGTACAGTCTT 1680
1800 GTATTACATTGTTTAAATAAGTCAATGATAAACTTAAAAAAGGAGGAGGAGGAGGAGGAG 1859
1681 GTATTACATTGTTTAAATAAGTCAATGATAAACTTAAAAAAGGAGGAGGAGGAGGAGGAG 1740
1860 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1877
1741 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1758

RESULT 2
US-09-104-063-3
; Sequence 3, Application US/09104063
; Patent No. US20020168356A1
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,063
; FILING DATE: 24-June-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/701265
; FILING DATE: 22-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/664228
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-104-063-3

Query Match 51.9%; Score 974.4; DB 3; Length 1737;
Best Local Similarity 76.1%; Pred. No. 3.4e-211;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

QY 50 GCAGGTAGCAGTACCTCTGAGGCGTTGGTGTCTCGGTAAACACACCGGCTGTAGAGC 109
DB 20 GCAGGCGGCAAGAGTGACGCGGAGGCGCTGAGTGTCTCCAGTAGCACCGCATCTGGAGAAC 79
QY 110 GAGTGTGGCCATGGAACCGCATGAGTGTGAGTATATACACTTCTGATAACTACTCTGAAGA 169
DB 80 CAGCGTTACCATGGA-----GGGGATCAGTATATACACTTCTGATAACTACTACTACCGAGGA 134
QY 170 AGTGGGGCTCTGGAGACTATGACTCCAAAGGAACCTGTCTCCGGGATGAAACCGTCCA 229
DB 135 AATGGGCTCAGGGGACTATGACTCCATGAAGGAACCTGTCTCCGTGAAGAAATGCTAA 194
QY 230 TTTCATAGAGTCTTCTGCGCCACCATCTACTCATCATCTTCTTGACTGGCATAGTCCG 289
DB 195 TTTCATAGAGTCTTCTGCGCCACCATCTACTCATCATCTTCTTAACCTGGCATTTGGGG 254
QY 290 CAATGAGTGGTGTATCTGCTGATGGTGTACAGAGAGAGTAAAGGAGCATGACGACAA 349
DB 255 CAATGAGTGGTGTATCTGCTGATGGTGTACAGAGAGAGTAAAGGAGCATGACGACAA 314
QY 350 GTACCGGCTCAGCTGTGAGTGGTGTACCTCTCTTTGTATCATCACACTCCCTCTCTGGGC 409
DB 315 GTACCGGCTCAGCTGTGAGTGGTGTACCTCTCTTTGTATCATCACACTCCCTCTCTGGGC 374
QY 410 AGTTGATGCCATGGTGTGATCTGTTGGGAAATTTTGTGTAAAGCTGTGCTCATATCAT 469
DB 375 AGTTGATGCCATGGTGTGATCTGTTGGGAAATTTTGTGTAAAGCTGTGCTCATATCAT 434
QY 470 CTACACTGTCAACTCTACAGCAGCTGTCTCATCTGGCCCTTCATCAGCTGTGACCGGTA 529
DB 435 CTACAGCTCAACTCTACAGCAGCTGTCTCATCTGGCCCTTCATCAGCTGTGACCGGTA 494
QY 530 CTTGCGCATTTGTCCAGCCACCAACAGTCAAGGCCAAGGAAACTGTGCTGAAAGGC 589
DB 495 CTTGCGCATTTGTCCAGCCACCAACAGTCAAGGCCAAGGAAACTGTGCTGAAAGGC 554
QY 590 AGTCTATGTGGGCTGTGGATCCAGCCCTCTCTGACTATATACCTGACTTTCATCTTTC 649
DB 555 GGTCTATGTGGGCTGTGGATCCAGCCCTCTCTGACTATATCCGACTTTCATCTTTC 614
QY 650 CGAGCTCAGCCAGGGGACATCAGTCAAGGGGATGACAGTATCATCTGTGACCGCTTTA 709
DB 615 CAACG-----TCAGTAGGAGATGACAGATATATCTGTACCGCTCTA 659
QY 710 CCCCGATAGCTGTGGATGGTGTGTTTCAATTTCCAGCATATATAGTGGGTCTCATCTCT 769
DB 660 CCCCAATGACTGTGGGTGGTGTGTTTCCAGTTTCCAGCATATATAGTGGGTCTCATCTCT 719
QY 770 GCCCGGATCGTCTCTCTCTGTTTACATCATCATCTCTAAGCTGTCACTCCAA 829
DB 720 GCCTGGTATTGTCTATCTCTCTCTGTTTACATCATCTCTAAGCTGTCACTCCAA 779
QY 830 GGGCCACCAAGCGGAGCCCTCAAGACGACGATCATCTCTAGCTTTCTTTGC 889
DB 780 GGGCCACCAAGCGGAGCCCTCAAGACGACGATCATCTCTAGCTTTCTTTGC 839

RESULT 3
US-10-666-689-3
; Sequence 3, Application US/10666689

QY 890 CTCCTGCTGCCATATATATGTGGGATCAGCATCGACTCTTCTCATCTCTTTTGGAGTCAT 949
DB 840 CTGTTGGCTGCTTACTACATTGGGATCAGCATCGACTCTTCTCATCTCTCGGAAATCAT 899
QY 950 CAAGCAAGGATGTGACTTCCGAGAGCATTTGCAAGAGTGGATCTCCATCAGAGGCGCT 1009
DB 900 CAAGCAAGGATGTGAGTTTGAGAACACTGTGCAAGAGTGGATTTCCATCAGAGGCGCT 959
QY 1010 CGCTTTCTTCCACTGTGTGCTGAAACCCCATCTCTATGCTTCTCGGGGCCAAGTTCAA 1069
DB 960 AGCTTTCTTCCACTGTGTGCTGAAACCCCATCTCTATGCTTCTTGGAGCCAAATTTAA 1019
QY 1070 AGCTCTGCCAGCATGCACTCAATCCATGAGAGAGGCTCCAGCTCCAGCTCAAGATCTTTC 1129
DB 1020 AACCTCTGCCAGCAGCATCTACCTCTGTGAGCAGAGGCTCCAGCTCAAGATCTCTCTC 1079
QY 1130 CAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1189
DB 1080 CAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1139
QY 1190 CTCAGCTAACCTTATGCAAGAGCTTATATATATATATATATATATATATATATATATAT 1249
DB 1140 CTCAGCTAA-----CACAGATGTAAAGAGCTTTTATATACGATAAATTAATCTTTT 1191
QY 1250 TTTTATGTTACATTTTCCAGATATAAGAGACTGACCTGTTGACAGTCTTGTACAGTCTTTT 1309
DB 1192 TTTTAAAGTTTACATTTTTCAGATATAAAGAGACTGACCAATATGTTACAGTCTTTTATTGC 1251
QY 1310 TTTTAAAGTTTACAGTGTGGGAGTTTATGTTCTCTAGTCTTGTGAGGTTTGTAGCTTAAT 1369
DB 1252 TTGTTGGATTTTGT-----CTTGTGTTCTTGTGTTTGTGTTGTTGTTGTTGTTGTTGTT 1305
QY 1370 ATATAAATATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 1429
DB 1306 TTTATA-----TAAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 1361
QY 1430 AAGTTCTTAGTGTGTTTATCTGTGTAGGACTGTAGAACTGTAGAGGAGGAACTGA 1489
DB 1362 AAGTTCTTAGTGTGTTTATCTGTGTAGGACTGTAGAA-----AAGGGAAGTGA 1413
QY 1490 ACATTCAGAGTGTGGTAAATTAAGTAAAGTGTAGGACTGTAGGAGGAGGAGGAGGAGGAG 1549
DB 1414 ACATTCAGAGGCTGTAGTAAATCAGTAAAGTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1473
QY 1550 TAATCTTCTCATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1609
DB 1474 TAGATTAATCTCTCA-----1488
QY 1610 TGTGTTGTTTATGCTGTGTGATGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTT 1669
DB 1489 -----TTCCCGTGGAAACGTTTTCCTGTTCTTAAAGACGTTGAT 1525
QY 1670 TTTTCTGTAAGATGGCATTAACCAAGCTGAAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1729
DB 1526 TTTGCTGTAGAGATGGCATTAACCAAGCTGAAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1581
QY 1730 TTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1789
DB 1582 -----TTTTTCAGTTTTCAGGAGTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1623
QY 1790 GTACAGCTCTGTATTAATTTTAAAGTCAATGATTAAGTCAATGATTAAGTCAATGATTAAGT 1849
DB 1624 GTACAGCTCTGTATTAAGTCTTAAAGTCAATGATTAAGTCAATGATTAAGTCAATGATTAAGT 1683
QY 1850 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1877
DB 1684 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1711

Publication No. US20040037830A1

GENERAL INFORMATION:

APPLICANT: Wood, William I.

TITLE OF INVENTION: Human PF4A Receptors, Nucleic Acid Encoding and

FILE REFERENCE: P0706P2C2D2C1

CURRENT APPLICATION NUMBER: US/10/666,689

PRIOR FILING DATE: 2003-09-19

PRIOR APPLICATION NUMBER: US 09/104,063

PRIOR FILING DATE: 1988-06-24

PRIOR APPLICATION NUMBER: US 08/701,265

PRIOR FILING DATE: 1996-08-22

PRIOR APPLICATION NUMBER: US 08/664,228

PRIOR FILING DATE: 1996-06-06

PRIOR APPLICATION NUMBER: US 08/076,093

PRIOR FILING DATE: 1993-06-11

PRIOR APPLICATION NUMBER: US 07/810,782

PRIOR FILING DATE: 1991-12-19

PRIOR APPLICATION NUMBER: US 07/677,211

PRIOR FILING DATE: 1991-03-29

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 3

LENGTH: 1737

TYPE: DNA

ORGANISM: Homo sapien

US-10-666-689-3

Query Match 51.9%; Score 974.4; DB 7; Length 1737;

Best Local Similarity 76.1%; Pred. No. 3.4e-211;

Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

QY 50 GCAGGTAGCAGTACACCTCTGAGGCGTTTGGTCTCCGGTAAACCAACCGGCTGAGAC 109
DB 20 GCGCGCGCAAGTGAACGCGGAGGCGCTGAGTCTCCAGTAGCCACCGCATCTGGAGAAC 79
QY 110 GAGTGTGGCATGGAAACCGATCAGTGTGAGTATATACATCTCTGATAAATCTACTCTGAAGA 169
DB 80 CAGCGTTTACCATGGA-----GGGGATCAGTATATACATCTCAGATTAATCTACACCGGGA 134
QY 170 AGTGGGGTCTGGAGATATGACTTCCAAAGGAACCTGTCTCCGGATGAACACGTCCA 229
DB 135 AATGGGCTCAGGGGATATGACTTCCATGAAGGAACCTGTCTCCGTGAAGAAAATGCTAA 194
QY 230 TTTCAATAGATCTTCTCGCCACCACTACTTTCATCATCTCTTCTGATGGCATATCGG 289
DB 195 TTTCAATAAATCTTCTCGCCACCACTACTTTCATCATCTTCTTAACTGGCATTTGGG 254
QY 290 CAATGGATTGGTATCTGTGTCATGGTTTACCAAGAAAGCTAAGGAGCATGACGGACAA 349
DB 255 CAATGGATTGGTATCTGTGTCATGGTTTACCAAGAAAGCTAAGGAGCATGACGGACAA 314
QY 350 GTACCGGCTGACCTGTGTCAGTGTGACCTCTCTTTTGTGCATCACAATCCCTTCTGGGC 409
DB 315 GTACAGGCTGACCTGTGTCAGTGTGACCTCTCTTTGTGCATCAGCGTTCCCTTCTGGGC 374
QY 410 AGTTGATGCCATGGCTGACTGTGTTTGGGAAATTTTGTGTAAGGCTGTGTCATATCAT 469
DB 375 AGTTGATGCCATGGCTGACTGTGTTTGGGAAATTTTGTGTAAGGCTGTGTCATATCAT 434
QY 470 CTACACTGTCAACCTCTACAGCAGCGTTTCTCATCTCGGCCCTTCTCATCGCCCTGACCGGTA 529
DB 435 CTACAGATCNACTCTACAGCAGTGTCTCTCATCTCGGCCCTTCTCATCGTCTGACCGCTA 494
QY 530 CTTCCGCAATGTCCAGCCCAACCAAGTCAAGGCCAAGGAACTGTGTGCTGCTGAAAGGC 589
DB 495 CTTGGCCATCGTCCAGCCCAACCAAGTCAAGGCCAAGGAACTGTGTGCTGCTGAAAGGT 554
QY 590 AGTCTATGTGGGCTGTGGATCCAGCCCTCTCTGACTATATACCTGACTTCTATCTTTC 649
DB 555 GGTCTATGTGGGCTGTGGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
QY 650 CGACGTGAGCCAGGGGACATCAGTCAGGGGGATGACAGGTATCATCTGTGACCGCCTTTA 709

DB 615 CAACG-----TCAGTGAGGCAGATGACAGATATATCTGTGACCGCTTCTA 659
QY 710 CCCGATAGCCTGTGGATGGTGGTGTTCATATTCAGCATATAAATGGTGGTCTCATCT 769
DB 660 CCCCAATGACTTGTGGTGGTGGTGTTCAGTTCAGCACATCATGTTGGGCTTATCT 719
QY 770 GCGCGGATCGTCACTCTCTCTGTGTACTGTGATCATCATCTCTAAAGCTGTCACTCCAA 829
DB 720 GCTGGTATGTCACTCTCTGTCTGTCTATTTGATATCATCTCCAGCTGTCACTCCAA 779
QY 830 GGGCCACCAAGAGCGAAGCGCCTCAAGACAGAGTCACTCTCATCTAGCTTTCTTTGC 889
DB 780 GGGCCACCAAGAGCGAAGCGCCTCAAGACCAAGTCACTCTCTCATCTCTGGAATCAT 839
QY 890 CTGCTGGCTGCCATATATATGTGGGATCAGCATCTCTCTCTCTCTCTCTCTCTCTCT 949
DB 840 CTGTTGGCTGCCATATATATGTGGGATCAGCATCTCTCTCTCTCTCTCTCTCTCTCT 899
QY 950 CAAGCAAGGATGTGACTTCGAGAGCATTTGTGCAAGTGGATCTCCATCAGAGAGCCCT 1009
DB 900 CAAGCAAGGATGTGACTTCGAGAGCATTTGTGCAAGTGGATTTCCATCAGAGAGCCCT 959
QY 1010 CGCTTTCTTCCATCTGTGTGCTGAAACCCCATCTCTATGCTCTCTCTCTCTCTCTCTCT 1069
DB 960 AGCTTTCTTCCATCTGTGTGCTGAAACCCCATCTCTATGCTCTCTCTCTCTCTCTCTCT 1019
QY 1070 AGCTTTCTTCCATCTGTGTGCTGAAACCCCATCTCTATGCTCTCTCTCTCTCTCTCTCT 1129
DB 1020 AACCTCTGCGGATGAGCATCTCACTCTCTGAGCAGAGGCTCCAGCTCAAGATCTCTCT 1079
QY 1130 CAAAGAAAGCGGGTGGACACTCTTCTCTCTCCAGGAGTCAAGTCTCTCAGATTTTCA 1189
DB 1080 CAAAGAAAGCGAGTGGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1139
QY 1190 CTCCAGCTAACCTTATGCAAGACTTATATATATATATATATATATATATATATATAT 1249
DB 1140 CTCCAGCTAACCTTATGCAAGACTTATATATATATATATATATATATATATATATAT 1191
QY 1250 TTTTATGTTTACACATTTTCCAGATATAGAGACTGACAGTCTCTGACAGTCTTTTCTT 1309
DB 1192 TTTTATGTTTACACATTTTCCAGATATAGAGACTGACAGTCTCTGACAGTCTTTTCTT 1251
QY 1310 TTTTATGTTTACACTTTTGGGAGTTTATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1369
DB 1252 TTTTATGTTTACACTTTTGGGAGTTTATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1305
QY 1370 ATATAAATATGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1429
DB 1306 TTTATA-----TAAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1361
QY 1430 AAGTTCTTAGTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1489
DB 1362 AAGTTCTTAGTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1413
QY 1490 ACATTCAGAAATGTGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1549
DB 1414 ACATTCAGAAATGTGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1473
QY 1550 TAATCTCTTCAATTCGAGGAGCACCACCCCAACCCCAACCCCAACCCCAACCCCAACCT 1609
DB 1474 TAGATAATCTCTCA-----TTCCTGTTGAAACCTTTTCTGTTCTTAAAGACGTGAT 1488
QY 1610 TGTGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1669
DB 1489 -----TTCCTGTTGAAACCTTTTCTGTTCTTAAAGACGTGAT 1525
QY 1670 TTTTCTGTTAAAGATGGCATTAAAAACCAAGCCTGAAATGGTGGTAGAAATGCTGGGT 1729
DB 1526 TTTGCTGTAGAGATGGCATTAAAAACCAAGCCTGAAATGGTGGTAGAAATGCTGGGT 1581
QY 1730 TTTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1789

Qy 1664 TTTTITTTTTCTGTAAAGATGGCACATTAAAA CAAAGACCTGAAATGGTGGTGAAGATGC 1723
Db |||||
1535 CGTGATTTTCTGTAGAAGATGGCACATTAAACCAGAGCCAAAGTGGT-ATAGAAATGC 1593
Qy 1724 TGGGTTTTTTTTTGTGTTGTTGTTTTTTCAGTTTTCAGAGTAGATGACTTCAGTCCCT 1783
Db |||||
1594 TGG-----TTTTTCAGTTTTCAGGAGTGGGTTGATTTTCAGCACCT 1633
Qy 1784 ACAAAATGACAGTCTTGTTATTTACATTTGTTAATAAAAGTCAATATAAACTTTAAAAAATA 1843
Db |||||
1634 AC-AGTGTACAGTCTTGTTATTTAGTTGTTAATAAAGTACATGTTAAACTTTAAAAAATA 1692
Qy 1844 AAAAAAAAAAAAAAAAAAAAAA 1865
Db |||||
1693 AAAAAAAAAAAAAAAAAAAAAA 1714

RESULT 5
US-10-775-920-373
; Sequence 373, Application US/10775920
; Publication No. US2004017544A1
; GENERAL INFORMATION:
; APPLICANT: Mergen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; FILE REFERENCE: Mergen - 0010B
; CURRENT APPLICATION NUMBER: US/10/775,920
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 373
; LENGTH: 1699
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-920-373

Query Match 51.4%; Score 964.2; DB 8; Length 1699;
Best Local Similarity 75.7%; Pred. No. 7.1e-209;
Matches 1385; Conservative 0; Mismatches 208; Indels 136; Gaps 10;

Qy 37 CGCCCGGCGCAGGTGCAGGTAGCAGTACCCCTCTGAGGCGTTTGGTGTCTCGGTAAACCACC 96
Db 7 CGTCCGCGACGCGTGGCGGACGCGTGGGGCCGAGGCGCTGAGTGTCCAGTAGCCACC 66
Qy 97 ACGGCTGTAGAGCAGGTGTTGCCATGAAACCGATCAGTGTGAGTATATACATTTCTGATA 156
Db 67 GCATCTGGAGAACCCAGCGGTTTACCATGGA-----GGGGATCAGTATATACATTTGATA 121
Qy 157 ACTACTCTGAGAGTGGGCTGGAGCATATGACTCCACAGGACCCCTGCTCCGGG 216
Db 122 ACTACCGAGGAAATGGGCTCAGGGACATGACTCCATGAGGAAACCCCTGTTTCCGTG 181
Qy 217 ATGAAAACGTCATTTCAATAGGATCTTCTGCCACCATCTACTTCATCATCTTTTGA 276
Db 182 AAGAAATGCTAATTTCAATAAATCTTCTGCCACCATCTACTTCATCATCTTTCTAA 241
Qy 277 CTGGCATAGTCGGCAATGGATTTGGTGTATCTTGGTTCATGGGTTACGAGAAAGCTAAGGA 336
Db 242 CTGGCATTTGGGCAATGGATTGGTTCATCTTGGTTCATGGGTTACGAGAAAGCTAAGGA 301
Qy 337 GCATGACGACAGTACGGGCTGACCTGTGCTGAGTGGCTGACCTCTTGTGTATCATCAC 396
Db 302 GCATGACGACAGTACAGGCTGACCTGTGCTGAGTGGGCGACCTCTTGTGTATCATCAC 361
Qy 397 TCCCTTCTGGGCAAGTTGATGCCATGGCTGACTGCTTGTGGGAAATTTTGTGTAAAG 456
Db 362 TTCCCTTCTGGGCAAGTTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCTATGCAAG 421
Qy 457 CTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCGTTTCTCATCTGGCCTTCATCA 516

Qy	1597	CCCAATCTTAAATTGTTGGTTATGCTGTGTGANGTTTGTTGGTTTTGTTGGTTTTTTTTTTGTTGTT	1656
Db	1489	-----TTCCCGTGAACGTTTTTTTCCTGTT	1512
Qy	1657	GTTGTTGTTTTTTTTCTGTAAAAGATGGCACCCTTAACAACCAAAGCCTTGAATGGTGTA	1716
Db	1513	CTTAAGACGTCATTTGCTGTAGAAGATGGCACCTTATAACCAAAGCCAAAGTGT-ATA	1571
Qy	1717	GAATAGCTGGGGTTTTTTTTTGTGTTGTTTTTTCAGTTTTCAGAGTAGATTGACTTC	1776
Db	1572	GAATGCTGG-----TTTTTTCAGTTTTCAGAGTGGGTTGATTTTC	1611
Qy	1777	AGTCCCTACAATGTACAGTCTTGTATTTACATTTGTTAATAAAAGTCAATGATAAACTTAA	1836
Db	1612	AGCACCTAC-AGTGACAGTCTTGTATTAAAGTGTGTTAATAAAAGTACATGTATAAACTTAA	1670
Qy	1837	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1865
Db	1671	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1699
 RESULT 6 US-10-706-265-11 ; Sequence 11, Application US/10706265 ; Publication No. US20040132642A1 ; GENERAL INFORMATION: ; APPLICANT: Hwang, Sam ; TITLE OF INVENTION: METHODS OF INHIBITING METASTASIS OR GROWTH OF A TUMOR CELL ; FILE REFERENCE: 224738 ; CURRENT APPLICATION NUMBER: US/10/706,265 ; CURRENT FILING DATE: 2003-11-12 ; PRIOR APPLICATION NUMBER: 60/425,472 ; PRIOR FILING DATE: 2002-11-12 ; PRIOR APPLICATION NUMBER: 60/511,581 ; PRIOR FILING DATE: 2003-10-15 ; NUMBER OF SEQ ID NOS: 11 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 11 ; LENGTH: 1662 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-706-265-11			
 Query Match 51.2%; Score 960.4; DB 7; Length 1662; Best Local Similarity 76.3%; Pred. No. 5.1e-208; Matches 1371; Conservative 0; Mismatches 291; Indels 136; Gaps 10;			
Qy	68	CTGAGGCGTTTGGTGCTCCGGTAAACACACACCGGCTGTAGAGCGAGTGTGCCATGGAACC	127
Db	1	CCGAGGGCCTGAGTGCTCCAGTAGCCACCGCATCTGGAGAACACGCGGTACCATGGA--	58
Qy	128	GATCAGTGTGAGTATATACATTTCTGTATACTTCTGAAAGAGTGGGGTCTGGAGACTA	187
Db	59	---GGGGATCAGTATATACATTTCAGATAACTACACCAGGAAATGGGCTCAGGGGACTA	115
Qy	188	TGACTCCAAACAAGNACCCCTGCTCCGGGATGAAACCTGCATTTCAATAGATCTTCCT	247
Db	116	TGACTCCAATGAAGAACCCCTGTTCCCGTGAAGAAATGCTAATTTCAATAAAATCTTCCT	175
Qy	248	GCCCACCATCTACTTCAATCATCTTCTTCAGCTGGCATAGTCGGCAATGGATGGTGATCCT	307
Db	176	GCCCCACCATCTACTCCATCATCTTCTTAACCTGGCATTTGTGGCAATGGATGGTCATCCT	235
Qy	308	GGTCATGGGTTACAGAAAGAGCTAAAGAGCATGACGCAAGTACCCGGCTGCACCTGTC	367
Db	236	GGTCATGGGTTTACCAGAAAGAACTGAGAGGATGACGCAAGTACAGGCTGCACCTGTC	295
Qy	368	AGTGGCTGACCTCCTCTTTGTTCATCACACTCCCTTCTTGGGCGAGTTGATGCCATGGCTGA	427
Db	296	AGTGGCGACCTCTCTTTGTTCATCACGCGCTTCCCTTCTTGGGCGAGTTGATGCCGTTGCAAA	355
Qy	428	CTGTACTTTTGGGAAATTTTTTGTGTGAAGCGTGTCCATATCATCTACACTGTCAACCTCTA	487

Db	1395	TGAATCAGTAAGACTAGAATGATCCCGAGCTGTTTATGCAATAGATAATCTCTCCA	---	1451
Qy	1568	GAGCACCCACCCACCCACCCACCCACCCATTTCTAAATTTGTTGGTTATGCTGTGT		1627
Db	1452	-----		1451
Qy	1628	GATGGTTTGGTTTGGTTTGGTTTGGTTGTTGTTGTTTCTGTAAAGATGCC		1687
Db	1452	-----TTCCCGTGAACGTTTTTCTCTTAAGACGTGATTTTGTCTAGAGATGCC		1506
Qy	1688	ACTTAAACCAAAAGCCCTGAATGGTGTAGAAAATGCTGGGGTTTTTTTTTGTGTTTGT		1747
Db	1507	ACTTATAACCAAGCCCCAAGTGT-ATAGAAATGCTG-----	-T	1545
Qy	1748	TTTTCAAGTTTCAAGAGTAGAATGACTTTCAGTCCCTACAAATGACAGTCTGTATTACA		1807
Db	1546	TTTTCAAGTTTTCAGGAGTGGGTTGATTTTCAGCACCTAC-AGTGTACAGTCTGTATTAA		1604
Qy	1808	TTGTTAATAAAAGTCAATGATATAACTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA		1865
Db	1605	TTGTTAATAAAGTACATGTTAAACTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA		1662
RESULT 7				
US-10-151-274-14				
; Sequence 14, Application US/10151274				
; Publication No. US20030064071A1				
; GENERAL INFORMATION:				
; APPLICANT: Littman, Dan R.				
; APPLICANT: Kwon, Douglas S.				
; APPLICANT: van Kooyk, Yvette				
; APPLICANT: Geljtenbeck, Tneo				
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY				
; TITLE OF INVENTION: INTO				
; TITLE OF INVENTION: CELLS				
; FILE REFERENCE: 1049-1-017				
; CURRENT APPLICATION NUMBER: US/10/151,274				
; CURRENT FILING DATE: 2002-05-20				
; PRIOR APPLICATION NUMBER: US/09/517,605				
; PRIOR FILING DATE: 2000-03-02				
; NUMBER OF SEQ ID NOS: 17				
; SOFTWARE: PatentIn Ver. 2.0				
; SEQ ID NO 14				
; LENGTH: 1679				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-10-151-274-14				

[illegible]

Db 1354 GTGCCAAGTCTTAGTTGCTGTATGTCTCGTGGTAGGACTGTAGAA-----AAGG 1405
 Qy 1484 AACTGAACATCCAGAAATGTTGGTAAATGAATAAAGCTAGCGGTGATCCTCAGCTGTT 1543
 Db 1406 AACTGAACATCCAGAGCGTGTAGTGAATCAGCTAAAGCTAGAAATGATCCCCAGCTGTT 1465
 Qy 1544 GCTGCATA 1551
 Db 1466 TATGCATA 1473

RESULT 8

US-10-225-567A-75
 ; Sequence 75, Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LifeSpan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Burner, Glenna C.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 75
 ; LENGTH: 1679
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-225-567A-75

Query Match 50.8%; Score 952.8; DB 5; Length 1679;
 Best Local Similarity 80.28; Pred. No. 2.8e-206;
 Matches 1210; Conservative 0; Mismatches 252; Indels 46; Gaps 6;

Qy 44 GCAGGTGCAGGTAGCAGTACCTCTGAGCGTTGGTGTCCGGTAAACACACCGCTG 103
 Db 12 GCGGACGAGTAGCAAGTGAACGCGGAGGCGCTGAGTGTCCAGTAGCCACCGCATCTG 71
 Qy 104 TAGAGCGAGTGTGCCATGGAACGGATCAGTGTAGTATATACATCTCTGATACTACTC 163
 Db 72 GAGAACCGAGCGGTACCATGGA-----GGGGATCAGTATATATACATCTCAGATACTAC 126
 Qy 164 TGAAGAAGTGGGTCTCGAGACTATGACTCCAAACAGGAACCCCTGCTCCGGATGAATA 223
 Db 127 CGAGGAATGGGTCTAGGGAGCTATGACTCCATGAAGGAACCCCTGTTCCGTGAAGAAA 186
 Qy 224 CGTCCATTTCAATAGGATCTTCTGCCACCATCTACTTCATCATCTTCTTTGACTGGCAT 283
 Db 187 TGCTAAATTCATATAAATCTTCTGCCACCATCTACTTCATCATCTTCTTTAATGGCAT 246
 Qy 284 AGTCGGAATGGAATGGTGTATCTGTGTCATGGTTACCAAGAGAGCTAAGAGCATGAC 343
 Db 247 TGTGGGCAATGGAATGGTGTATCTGTGTCATGGTTTACCAAGAGAACTGAGAGAGCATGAC 306
 Qy 344 GGACAAAGTACCGGTCGACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 403
 Db 307 GGACAAAGTACCGGTCGACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 366
 Qy 404 CTGGGCAATGATGCCATGGCTGACTGTGTAATTTGGGAAATTTTGTGTAAGCTGTCCA 463
 Db 367 CTGGGCAATGATGCCATGGCTGACTGTGTAATTTGGGAAATTTTGTGTAAGCTGTCCA 426
 Qy 464 TATCATCTACACTGTCAACCTCTACAGCAGGTTCTCATCTCGGCTTCTCATCGCCTGGA 523
 Db 427 TGTCACTACACAGTCAACCTCTACAGCAGTGTCTCATCTCGGCTTCTCATCGCCTGGA 486
 Qy 524 CCGGTACTCGCCATGTTGTCCACGCCACCAACAGTCAAGGCCAAGGAACTGTGCTGA 583
 Db 487 CCGGTACTCGCCATGTTGTCCACGCCACCAACAGTCAAGGCCAAGGAACTGTGCTGA 546

RESULT 9
 US-10-021-660-58
 ; Sequence 58, Application US/10021660

Qy 584 AAAGGCAAGTCTATGTGGGCGTCTGGATCCAGAGCCCTCTCTCTGACTATATACCTGACTTTCAT 643
 Db 547 AAAGTGGTCTATGTGGGCGTCTGGATCCAGAGCCCTCTCTCTGACTATATACCTGACTTTCAT 606
 Qy 644 CTTTGGCCGAGCTCAGCCAGGGGACATCAGTCAAGGGGATGACAGGTACATCTGTGACCG 703
 Db 607 CTTTGGCAAG-----TCAGTGAAGGAGATGACAGATATATCTGTGACCG 651
 Qy 704 CTTTATACCCGATAGCTGTGGATGGTGGTGTTCATATCCAGCATATATATGGTGGGTCT 763
 Db 652 CTTTATACCCCAATGACTGTGGGTGGTGTTCAGATTTTTCAGCATATATATGGTGGGTCT 711
 Qy 764 CATCTGCGCGGATCGTCACTCTCTCTGTTACTGTGATCATCATCTCTAAGCTGTGACCA 823
 Db 712 TATCTCTGCTGTGTTATGTCATCTCTCTGTTACTGTCATCATCTCTCAAGCTGTGACCA 771
 Qy 824 CTCGAAGGCGCCACCAAGCGCAAGGCCCTCAAGACGACAGTCACTCTCATCTCTAGCTTT 883
 Db 772 CTCGAAGGCGCCACCAAGCGCAAGGCCCTCAAGACGACAGTCACTCTCATCTCTGCTTT 831
 Qy 884 CTTTGGCTGTGCTGCCATATTTATGTGGGGATCAGCATCGACTCTCTCATCTCTTTGGG 943
 Db 832 CTTTGGCTGTGCTGCCATTTACTACATTTGGGATCAGCATCGACTCTCTCATCTCTTGA 891
 Qy 944 AGTCATCAAGCAAGGATGTGACTTCAGAGCATTTGTGCAAGTGGATCTCTCATCATCAGA 1003
 Db 892 AATCATCAAGCAAGGATGTGAGTTTGAGAACACTGTGCAACAGTGGATTTCCATCATCCA 951
 Qy 1004 GGCCCTCGCTCTTCTCCAGTGTGCTGCAACCCCTCTCTATGCTCTCTCTCGGGGCCAA 1063
 Db 952 GGCCCTAGCTTCTTCCACTGTGTCTGAAACCCCTCTCTATGCTTTCTCTGGAGCCAA 1011
 Qy 1064 GTTCAAAAGCTCTGCCAGCATGCACTCAATCTCAGCAGAGGCTCCAGCTCTCAAGAT 1123
 Db 1012 ATTAAACCTCTGCCAGCAGCAGCTCACTCTGTGAGCAGAGGCTCCAGCTCTCAAGAT 1071
 Qy 1124 CTTTCCAAAGAAAGCGGGGTGGACACTCTCTCGTCTCCAGAGTCAAGATCTCTCCAG 1183
 Db 1072 CTTCTCCAAAGAAAGCGAGGTGGACATCTCTGTTTCCACTGAGTCTGAGTCTTCAAG 1131
 Qy 1184 TTTTCACTCCAGTAAACCTTATGCAAGACTTATATATATATATATATATATATATATAA 1243
 Db 1132 TTTTCACTCCAGTAAACAGAGTGTAAAGACTTTTT-----TTTATACATAATA 1183
 Qy 1244 GAATTTTATATGTTACACATTTTCCAGATATAAGAGACTGACCACTCTGTGACAGTTT 1303
 Db 1184 ACTTTTATAGTTACACATTTTTCAGATATAAAGACTGACCAATATTTGACAGTTT 1243
 Qy 1304 TTTTATTTTATTTGACTGTGGGAGTTTATGTTCTCTAGTTTGTGAGTGTGACT 1363
 Db 1244 TATTGCTTGTGGATTTTGT-----CTTGTGTTTCTTTAGTTTGTGAGTTTAAAT 1297
 Qy 1364 TAATTTATATAATATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 1423
 Db 1298 GACTTATTTATA-----TAAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 1353
 Qy 1424 GTGGCCAAAGTCTTGTAGTGTGTTTATCTGTGTGAGGACTGTAGAACTGTAGAGGAGA 1483
 Db 1354 GTGGCCAAAGTCTTGTAGTGTGTTTATCTGTGTGAGGACTGTAGAACTGTAGAGGAGA 1405
 Qy 1484 AACTGAACATTTCCAGAAATGTGGTAAATTTGAATAAAGCTAGCCGTGATCTCTCAGCTGTT 1543
 Db 1406 AACTGAACATTTCCAGAGCGTGTAGTGAATCAACAGTAAAGCTAGAAATGATCCCCAGCTGTT 1465
 Qy 1544 GCTGCATA 1551
 Db 1466 TATGCATA 1473

Publication No. US20030152926A1
 GENERAL INFORMATION:
 APPLICANT: Murray, Richard
 APPLICANT: Glynn, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: EOS Biotechnology, Inc.
 TITLE OF INVENTION: Compositions and Methods of Diagnosis of Angiogenesis,
 TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
 TITLE OF INVENTION: Modulators
 FILE REFERENCE: 018501-00071005
 CURRENT APPLICATION NUMBER: US/10/021,660
 CURRENT FILING DATE: 2001-12-06
 PRIOR APPLICATION NUMBER: US/09/784,356
 PRIOR FILING DATE: 2001-02-14
 PRIOR APPLICATION NUMBER: US 09/637,977
 PRIOR FILING DATE: 2000-08-11
 NUMBER OF SEQ ID NOS: 135
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 58
 LENGTH: 1679
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-021-660-58

Query Match 50.8%; Score 952.8; DB 6; Length 1679;
 Best Local Similarity 80.2%; Pred. No. 2.8e-206;
 Matches 1210; Conservative 0; Mismatches 252; Indels 46; Gaps 6;

QY 44 GCAGGTGCGAGGTAGCAGTACCCTCTGAGCGCTTTGGTGGCTCCGGTAACCAACCGCGGTG 103
 DB 12 GCGGCGAGCAGGTAGCAAGGTAGCGCGAGCGCTGAGTGTCTCAGTAGCCACCGCATCTG 71
 QY 104 TAGAGCAGGTGTTGCCATGGACCGATCAGTGTGAGTATATACATCTCTGATTAACCTAC 163
 DB 72 GAGAACGAGCGGTACCATGGA-----GGGGATCAGTATATATACATCTCAGATTAAC 126
 QY 164 TGAAGAGGTGGGTCTGGAGCATATGACTCCAAAGGAACCTGCTTCGGGATGAATA 223
 DB 127 CGAGGAATGGGCTCAGGGGACATGACTCCATGAGGAACCTGTTCCGTGAGGAATA 186
 QY 224 CGTCCATTTCAATPAGGATCTTCTGCGCCACCATCTACTTCATCATCTTCTTGACTGGCAT 283
 DB 187 TGTAAATTTCAATAAATCTCTGCGCCACCATCTACTTCATCATCTTCTTAACTGGCAT 246
 QY 284 AGTCGCAATGGATTTGGTATCTCTGCTGATGCTGCTGATGCTGATGCTGATGCTGATGCT 343
 DB 247 TGTGGCAATGGATTTGGTATCTCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 306
 QY 344 GGACAGTACCGGCTGCACCTGTGAGTGGCTGACCTCTCTTTGTCTATCATCATCTCCCTT 403
 DB 307 GGACAGTACAGGCTGCACCTGTGAGTGGCTGACCTCTCTTTGTCTATCATCATCTCCCTT 366
 QY 404 CTGGGCGAGTTGATGCCATGGCTGACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 463
 DB 367 CTGGGCGAGTTGATGCCGTTGGCAAACTGGTACTTTGGGAACCTCTCTATGCAAGGCGATCCA 426
 QY 464 TATCATCTACACTGTCAACCTCTACAGCAGCGTTCTCATCTGCGCTTCTATCATGCTGGA 523
 DB 427 TGTCACTACACAGTCAACCTCTACAGCAGTGTCTCATCTGCGCTTCTATCATGCTGGA 486
 QY 524 CCGGTACCTCGCATTTGTCTCAACGCCACCAACAGTCAAGGCCCAAGGAACCTGCTGGCTGA 583
 DB 487 CCGCTACCTGGCCATCTGTCTCAACGCCACCAACAGTCAAGGCCCAAGGAACCTGTTGGCTGA 546
 QY 584 AAAGGCGAGTCTATGTGGGCGTCTGGATGCCAGCCCTCTCTCTGACTATATACCTGACTTCAT 643
 DB 547 AAAGGCGGTCTATGTGGGCGTCTGGATGCCAGCCCTCTCTCTGACTATATCCCGACTTCAT 606
 QY 644 CTTTGGCGAGTCAAGCCAGGGGACATCATCATGAGGGGATGACAGGTACATCTCTGACCG 703
 DB 607 CTTTGGCAACG-----TCAGTGGGCGAGATGACAGATATATCTGTGACCG 651
 QY 704 CCTTTACCCCGATAGCTGTGGATGGTGGTGTTCATTTCAATTCAGCATATATGTGGGTCT 763

DB 652 CTTTACCCCAATGACTTGTGGTGGT 711
 QY 764 CATCTGCGCGGCGATCGTCTATCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 823
 DB 712 TATCTGCGCTGT 771
 QY 824 CTTCAAGGCCCAACCAAGGCCCTCAAGGCCCTCAAGGCCCTCAAGGCCCTCAAGGCCCTCAAGGCCCT 883
 DB 772 CTTCAAGGCCCAACCAAGGCCCTCAAGGCCCTCAAGGCCCTCAAGGCCCTCAAGGCCCTCAAGGCCCT 831
 QY 884 CTTTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
 DB 832 CTTTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891
 QY 944 AGTCATCAAGCAAGGATGTGACTTCGAGAGCATTTGTGCAAGGATGTGCAAGGATGTGCAAGGATGTG 1003
 DB 892 AATCATCAAGCAAGGATGTGACTTCGAGAGCATTTGTGCAAGGATGTGCAAGGATGTGCAAGGATGTG 951
 QY 1004 GCGCTCGCTTCTTCCACTGTTGCTGAACCCCTCTCTATGCTGCTCTCTGCTGCTGCTGCTGCTGCT 1063
 DB 952 GCGCTGAGCTTCTTCCACTGTTGCTGAACCCCTCTCTATGCTGCTCTCTGCTGCTGCTGCTGCTGCT 1011
 QY 1064 GTTCAAAAGCTCTGCGGAGCATGCACTCAACTCCATGAGCAGAGGCTCCAGGCTCAAGAT 1123
 DB 1012 ATTAAAGCTCTGCGGAGCATGCACTCAACTCTGTGAGCAGAGGCTCCAGGCTCAAGAT 1071
 QY 1124 CTTTCAAGGAAGCGGGTGGACACTCTTCCGCTCTCCAGGATCAGATCCTCCAG 1183
 DB 1072 CTTCTCAAGGAAGCGGGTGGACACTCTTCCGCTCTCCAGGATCAGATCCTCCAG 1131
 QY 1184 TTTTCACTCCAGTAACTTATGCAAGGATTTATATATATATATATATATATATATATATATATATATAA 1243
 DB 1132 TTTTCACTCCAGTAACTTATGCAAGGATTTATATATATATATATATATATATATATATATATATAA 1183
 QY 1244 GAACCTTTTATGTTACACATTTTCCAGATATAAGAGACTGACCAAGTCTGTGACAGTTT 1303
 DB 1184 ACTTTTATGTTTACACATTTTCCAGATATAAGAGACTGACCAAGTCTGTGACAGTTT 1243
 QY 1304 TTTTATTTTATGTTTACACATTTTCCAGATATAAGAGACTGACCAAGTCTGTGACAGTTT 1363
 DB 1244 TATGCTGTTGGATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1297
 QY 1364 TAATTATATAATATTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 1423
 DB 1298 GACTTATTTATA-----TAAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 1353
 QY 1424 GTGGCAAGTCTTATGTTAGTCTGTTTATCTGTGTGTTAGGACTGTGAGAACTGTGAGGAAGA 1483
 DB 1354 GTGGCAAGTCTTATGTTAGTCTGTTTATCTGTGTGTTAGGACTGTGAGAACTGTGAGGAAGA 1405
 QY 1484 AACTGCAACATCCAGATGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1543
 DB 1406 AACTGCAACATCCAGATGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1465
 QY 1544 GCTGCATA 1551
 DB 1466 TATGCATA 1473

RESULT 10
 US-10-170-385-332
 ; Sequence 332, Application US/10170385
 ; Publication No. US20030203372A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ward, Neil Raymond
 ; APPLICANT: Mundy, Christopher Robert
 ; APPLICANT: Kan, On
 ; APPLICANT: Harris, Robert Alan
 ; APPLICANT: White, Jonathan
 ; APPLICANT: Binley, Katie Mary
 ; APPLICANT: Rayner, William Nigel
 ; APPLICANT: Naylor, Stuart

Best Local Similarity 80.2%; Pred. No. 2.8e-206; Matches 1210; Conservative 0; Mismatches 252; Indels 46; Gaps 6;	
Qy	44 GCAGGTGCAGGTAGCAGTGCACCTCTCAGGCGTTTGGTGTCTCCGGTAACACCAACGCGCTG 103
Db	12 GCGCAGCAGGTAGCAAAAGTGCACGCCAGGCGCTGAGTGTCTCAGTAGCCACCGCATCTG 71
Qy	104 TAGAGCAGGTGTTGCCATGGAAACCGATCAGTGTGAGTATATACACTTCTGTAACTACTC 163
Db	72 GAGAACAGCGGTTTACCATGGA-----GGGGATCAGTATATACACTTTCAGATACTACAC 126
Qy	164 TGAAGAGTGGGCTCGAGGACTATGACTCCMACAAGGAACCCCTGCTTCGGGATGAAAA 223
Db	127 CGAGAAATGGGCTCAGGGGACTATGACTCATGAAGGAACCCCTGTTTCCGTGAAGAAAA 186
Qy	224 CGTCCATTTCAATAGGATCTTCTTCGCCACCATCTACTTTCATCATCTTCTTGTACTGGCAT 283
Db	187 TGTAAATTTCAATAAATCTTCTTCGCCACCATCTACTTCATCATCTTCTTAACTGGCAT 246
Qy	284 AGTCGGCAATGGATTTGTGTATCTCTGGTTCATGGGTTACCAAGAAGCTAAGGAGCATGAC 343
Db	247 TGTGGGCAATGGATTGCTCATCTCTGGTTCATGGGTTTACCAAGAAGCTGAGAAGCATGAC 306
Qy	344 GGCAGTACCGGCTGCACCTGTTCAGTGGCTGACCTCTCTTGTGTATCATCATCTCCCTT 403
Db	307 GGCAGAGTACAGGCTGCACCTGTTCAGTGGCGGCACTCTCTCTTGTGTATCATCGCTTCCCTT 366
Qy	404 CTGGCAGTTGTATGCCCATGGCTGACTGGTACTTTTGGGAAATTTTGTGTAAAGGCTGTCCA 463
Db	367 CTGGCAGTTGTATGCCCTGGCAAACTGGTACTTTTGGGAACTTCTTATGCAAGGCAATCCA 426
Qy	464 TATCATCTACACTGTCAACCTCTACAGCAGCGTTTCTCATCTCGGCCCTTCAATCAGCCTGGA 523
Db	427 TGTTCATCTACACAGTCAACTCTACAGCAGTGTCTCATCTCGGCCCTTCAATCAGTCTGGA 486
Qy	524 CCGGTACTCGCCATTTGTCAAGCCACCAAGTCAAGGCCAAGGAACTGTCTGGCTGA 583
Db	487 CCGGTACTCGCCCATCGTCCACGCGCACTCAACAGTCAAGGCCAAGGAACTGTGTGGCTGA 546
Qy	584 AAAGGCAGTCTATGTGGCGCTGTGGATCCAGAGCCCTCTCTGACTATATCCTGACTTTCAT 643
Db	547 AAAGTGGTCTATTTTGGCGCTGTGGATCCCTGCGCTCTGCTGACTATATCCCGACTTTCAT 606
Qy	644 CTTTGGCGAGTGCAGCCAGGGGGACATCAGTCAGGGGGATGACAGGTACATCTGTGACCG 703
Db	607 CTTTGGCAACG-----TCAGTGAAGGCAGATGACAGATATATCTGTGACCG 651
Qy	704 CTTTATCCCGATAGCCTGTGGATGTGTGGTGTTCATTTCCAGGATATAATGTGGGTCT 763
Db	652 CTTTCTACCCCAATGACTTGTGGGTGGTGTGTTCAGTTTTCAGTTCAGCACATCATGGTGGCCT 711
Qy	764 CATCTCTGCCGGCATCGTCATCTCTCTGTTACTGCATCATCATCTCTTAAGCTGTACA 823
Db	712 TATCTCTGCCCTGGTATGTGTATCTCTCTGCTATTTGCAATTATCATCTCCAAGCTGTACA 771
Qy	824 CTCCAAGGGCCACAGAAAGCGGAGCCCTCAAGACGACAGTCACTCTCATCTCTAGCTTT 883
Db	772 CTCCAAGGGCCACAGNAGCGCAAGGCCCTCAAGACCAAGTCACTCATCTCTGGCTTT 831
Qy	884 CTTTGGCTGTGGCTGCCATATTATTTGCGGATCAGCATCGATCTCTTCACTCTTTTGGG 943
Db	832 CTTTGGCTGTGGCTGCTTACTACATGGGATCAGCATCGATCTCTTCACTCTCTCTGGA 891
Qy	944 AGTCATCAAGCAGGATGTGACTTCGAGAGCATTTGTGCAAGTGGATCTCCATCACAGA 1003
Db	892 AATCATCAAGCAGGAGGTGTGAGTTTGAGAACTGTGCAAGTGGATTTCCATCACCGA 951
Qy	1004 GGCCTCTCGCCTTCTTCCACTGTGTGCTTGAACCCCATCTCTATGCTTCTCTGGGCGCAA 1063
Db	952 GGCCTTAGCTTCTTCCACTGTGTGTGAAACCCCATCTCTATGCTTCTCTGGAGCCAA 1011
Qy	1064 GTTCAAAGAGCTGTGCCAGCATGCATCAACTCCATGAGCAGAGGCTTCCAGCCTCAAGAT 1123

```

RESULT 13
US-10-211-462-80
; Sequence 80, Application US/10211462
; Publication No. US20040033495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis
; FILE REFERENCE: 018501-0062000S
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-211-462-80

```

	Query Match	50.8%;	Score 952.8;	DB 7;	Length 1679;
	Best Local Similarity	80.2%;	Pred. No. 2.8e-206;		
	Matches 1210;	Conservative	0;	Mismatches 252;	Indels 46; Gaps 6;
Qy	44	GCAGGTGCAGGTAGCAGTGCACCTCTCAGGCGCTTTGGTGTCCGGTAACCAACCAACCGGCTG	103		
Db	12	GCGGCAGCAGGTAGCAAGTGAGCCGAGGCGCTTGAGTGTCTCAAGTAGCCACCGCATCTG	71		

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QY 104 TAGAGCGAGTGTGGCCATGGAACCGATCAGTGTGAGTATATACATCTTCGATAACTACTC 163
DB 72 GAGAACACGCGGTACCATGGA-----GGGGATCAGTATATACATCTTCAGATTAACATAC 126
QY 164 TGAAGAAGTGGGGTCTGGAGACATATGATCTCAACAAGAAACCTGCTTCGGGATGAAA 223
DB 127 CGAGGAAATGGGCTCAGGGGACTATGACTCCATGAAAGAACCTGTTCGCTGAAGAAA 186
QY 224 CGTCCATTTCAATAGGATCTTCCTGGCCACCATCTACTTCATCATCTTCTTGATGGCAT 283
DB 187 TGTAAATTTCAATAAAATCTTCCTGGCCACCATCTACTTCATCATCTTCTTAACGGCAT 246
QY 284 AGTCGGCAATGGATTTGGTGTATCTGTGTCATGGTACCAGAAAGCTAAGAGGACATGAC 343
DB 247 TGTGGCAATGGATTTGGTGTATCTGTGTCATGGTACCAGAAAGCTAAGAGGACATGAC 306
QY 344 GGAACAAGTACCGGCTGCACCTGTCAAGGCTGACCTCTCTTTGTATCATCACTCCCTTT 403
DB 307 GGACAAGTACAGGCTGCACCTGTCAAGGCTGACCTCTCTTTGTATCATCACTCCCTTT 366
QY 404 CTGGGAGTTGATGCCATGGCTGACTGGTACTTTTGGGAAATTTTGTGTAAGGCTGTCCA 463
DB 367 CTGGGAGTTGATGCCATGGCTGACTGGTACTTTTGGGAAATTTTGTGTAAGGCTGTCCA 426
QY 464 TATCATCTACACTGTCAACCTCTACAGCAGGCTTCTCATCTCGCCCTTCATCAGCCTGGA 523
DB 427 TGTCACTACACAGTCAACCTCTACAGCAGGCTTCTCATCTCGCCCTTCATCAGTCTGGA 486
QY 524 CCGGTACTCTCGCCATTTGTCCACGCCACCAACAGTCAAGGCCAAGGAAATCTGTGGCTGA 583
DB 487 CGCTACTCTGGCCATCTGTCCACGCCACCAACAGTCAAGGCCAAGGAAATCTGTGGCTGA 546
QY 584 AAAGGAGTCTATGTGGGCTCTGATCTGATCTCCAGCCCTCTCTCTGACTATATCTGACTTCAT 643
DB 547 AAAGTGGTCTATGTGGGCTCTGATCTGATCTCCAGCCCTCTCTCTGACTATATCTCCGACTTCAT 606
QY 644 CTTTTCGGAGTCAAGCGGGGACATCAGTCAGGGGATGACAGGTACATCTGTGACCG 703
DB 607 CTTTTCGCAAG-----TCAGTGAGGAGATGACAGATATATCTGTGACCG 651
QY 704 CTTTACCCGATAGCTGTGGATGTGGTGTTCATTTCCAGCATATATATGTGGGTCT 763
DB 652 CTTTACCCGATAGCTGTGGTGTGGTGTTCAGTTTCCAGTTTCCAGCATATCTGTGGCT 711
QY 764 CATCTGCGCGGATGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 823
DB 712 TATCTCTGCTGTGTATGTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 771
QY 824 CTCGAAGGCGCACAGAGCGCAAGGCCCTCAAGACGACAGTCACTCTCATCTCTAGCTTT 883
DB 772 CTCGAAGGCGCACAGAGCGCAAGGCCCTCAAGACGACAGTCACTCTCATCTCTCTCTCT 831
QY 884 CTTTGTGCTGTGCTGCTGCTATATATGTGGGATCAGCATCGACTCTCTCTCTCTCTCTCT 943
DB 832 CTTTGTGCTGTGCTGCTGCTATATATGTGGGATCAGCATCGACTCTCTCTCTCTCTCTCT 891
QY 944 AGTCATCAAGCAAGATGTGACTTTCGAGAGCATTTGCAACAAGTGGATCTCTCATCAGAGA 1003
DB 892 AATCATCAAGCAAGAGGTGTGAGTTTGAGAACACTGTGTGCAACAAGTGGATTTCCATCA 951
QY 1004 GGCCTCTGCTCTTCTCACTGTGCTGCAACCCCATCTCTATGCTCTCTCTCTCTCTCTCT 1063
DB 952 GGCCTCTGCTCTTCTCACTGTGCTGCAACCCCATCTCTATGCTCTCTCTCTCTCTCTCT 1011
QY 1064 GTTCAAAAGCTCTGCCAGATGACTCAACTCCATCGAGCAGAGGCTCCAGCCTCAAGAT 1123
DB 1012 ATTTAAACCTCTGCCAGACGACTCACTCTCTGTGAGCAGAGGCTCCAGCCTCAAGAT 1071
QY 1124 CTTTTCGAAGGAAAGCGGGGTGAGACCTCTTGGTCTCTCAAGGATCAGAAATCTCTCCAG 1183
DB 1072 CTTCTCAAAAGGAAAGCGAGGTGAGACATTCATCTGTGTTCACACTGAGTCTGAGTCTTCAAG 1131
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QY 1184 TTTTCACTCCAGCTAACCCCTTATGCAAGACTTATATATATATATATATATATATATATATA 1243
DB 1132 TTTTCACTCCAGCTAACACAGATGTAAAGACTTTT-----TTTATACGATAAATA 1183
QY 1244 GAACCTTTTATGTGTACACATTTTCCAGATATAAGAGACTGACCACTGTTGTACAGTTT 1303
DB 1184 ACTTTTAAAGTTTACACATTTTCCAGATATAAAGACTGACCAATATTTGTACAGTTT 1243
QY 1304 TTTTATTTTAAATTAAGTGTGGGAGTTTATGTTCTCTAGTTTGTGAGGTTTGAAT 1363
DB 1244 TATGCTGTGGATTTTGT-----CTTGTGTTTCTTTAGTTTGTGAGGTTTAAAT 1297
QY 1364 TAATTATATAAATATTTTGTTTTGTTCATGTGAATGAGCGCTAGGCAGGACCT 1423
DB 1298 GACTTATTATA-----TAATTTTGTTCATATGATGTGTCTAGGCAGGACCT 1353
QY 1424 GTGGCCAAAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGACTGTAGAACTGTAGAGGAAGA 1483
DB 1354 GTGGCCAAAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGACTGTAGAA-----AAGGG 1405
QY 1484 AACTGAACATTTCCAGAACTGTGTTAAATTTGAATAAGCTAGCCGTGATCCTCAGCTGTT 1543
DB 1406 AACTGAACATTTCCAGAGCGTGTAGTGAATCAGTAAAGCTAGAAATGATCCCGCTGTT 1465
QY 1544 GCTGCATA 1551
DB 1466 TATGCATA 1473
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RESULT 14

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US-10-181-906-9
; Sequence 9, Application US/10181906
; Publication No. US20040053864A1
; GENERAL INFORMATION:
; APPLICANT: Karsenty, Gerard
; APPLICANT: Amling, Michael
; APPLICANT: Ducey, Patricia
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BONE FORMATION VIA
; TITLE OF INVENTION: MODULATION OF NEUROPEPTIDE Y ACTIVITY
; FILE REFERENCE: 9142-020-999
; CURRENT APPLICATION NUMBER: US/10/181,906
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/02040
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-181-906-9
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Query Match 50.8%; Score 952.8; DB 7; Length 1679;

Best Local Similarity 80.2%; Pred. No. 2.8e-206;

Matches 1210; Conservative 0; Mismatches 252; Indels 46; Gaps 6;

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QY 44 GCAGGTGTCAGGTAGCAGTCACTCTCGAGCGTTTGTGTCCTCGGTAACACACCGGCTG 103
DB 12 GCAGGTGTCAGGTAGCAGTCACTCTCGAGCGTTTGTGTCCTCGGTAACACACCGGCTG 71
QY 104 TAGAGCGAGTGTGGCCATGGAACCGATCAGTGTGAGTATATACATCTTCGATAACTACTC 163
DB 72 GAGAACACGCGGTACCATGGA-----GGGGATCAGTATATACATCTCAGATAACTACAC 126
QY 164 TGAAGAAGTGGGGTCTGGAGACTATGACTCCAAAGAAACCTGCTTCGGGATGAAA 223
DB 127 CGAGGAAATGGGCTCAGGGGACTATGACTCCATGAGGAACCTGTTTCCGTGAAGAAA 186
QY 224 CGTCCATTTCAATAGGATCTTCTGCTGCCACCATCTACTTCATCATCTTCTTGACTGGCAT 283
DB 187 TGTAAATTTCAATAAAATCTTCTGCTGCCACCATCTACTTCATCATCTTCTTAACCTGGCAT 246
QY 284 AGTCGGCAATGGATTTGGTGTATCTGTGCTGAGTGTACAGAGGCTAAGAGGACATGAC 343
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Db 247 TGTGGGCAATGGATTTGGTCACTCTGGTTCATGGGTTACCAAGAAGAACTGAGAGCATGAC 306
Qy 344 GGACAACTACCGGCTGCACTGTGAGGGTGCACCTCTCTTTGTTCATACACACTCCCCCTT 403
Db 307 GGACAACTACAGGCTGCACCTGTGAGGGCGGACCTCTCTTTGTTCATACAGCTCCCTT 366
Qy 404 CTGGGCAAGTTGATGCCATGCTGATCTGATCTTTGGGAAATTTTGTGTAAGGTGTCCA 463
Db 367 CTGGGCAAGTTGATGCCATGCTGATCTGATCTTTGGGAACTTCTTATGCAAGGCACTCCA 426
Qy 464 TATCATCTACACTGTCAACCTGTACAGCAGCTTCTCATCTGCGCTTCATCAGCCTGGA 523
Db 427 TGTCACTACACAGTCAACCTGTACAGCAGTGTCTCATCTGCGCTTCATCAGTCTGGA 486
Qy 524 CCGGTACTCTGCCATTTGTCACGCCCAACACAGTCAAGGCCAAGGAAACTGCTGGCTGA 583
Db 487 CCGTACTCTGCCATCTGTCACGCCCAACACAGTCAAGGCCAAGGAACTGTTGGCTGA 546
Qy 584 AAAGGCAAGTCTATGTTGGGCTGTGGATCCAGCCCTCTCTGACTATACCTGACTTCAT 643
Db 547 AAAGGTTGCTATGTTGGGCTGTGGATCCCTGCTGCTGACTATTCCTGACTTCAT 606
Qy 644 CTTTGGCGAGTCAAGCAGGCGGAGCATCACTCAGGGGATGACAGGTACATCTGTGACCG 703
Db 607 CTTTGGCAAGC-----TCAGTGAGGCGAGATGACAGATATATCTGTGACCG 651
Qy 704 CTTTACCCCGATAGCTGTGGATGGTGTGTTCAATTCAGCATATATGTTGGGTCT 763
Db 652 CTTTACCCCAATGACTTGTGGGTGGTGTGTTCCAGTTTCAGCATATATGTTGGCTT 711
Qy 764 CATCTGCCCGGATCGTCACTCTCTCTGTTACTGATCATCATCTTAAGCTGTGACA 823
Db 712 TATCTGCTGCTGATTTGTCACTCTGCTGCTGCTATTCATTCATCTCCAAGCTGCACA 771
Qy 824 CTCNAGGGCCACAGAGCGGAGGCTTCAAGCAGCATCATCTCATCTAGCTTT 883
Db 772 CTCNAGGGCCACAGAGCGGAGGCTTCAAGCAGCATCATCTCATCTAGCTTT 831
Qy 884 CTTTGGCTGCTGCTGCATTTATGTTGGGATCAGCATCGACTCTCTCATCTTTGGG 943
Db 832 CTTTGGCTGCTGCTGCTTACTACATTTGGGATCAGCATCGACTCTCTCATCTCTGGA 891
Qy 944 AGTCATCAAGCAAGATGTGACTTCGAGAGCATTTGTCACAAAGTGAATCTCCATCAAGA 1003
Db 892 AATCATCAAGCAAGGTTGAGTTTGAGAACACTGTGCAAAAGTGGATTTCCATCACCGA 951
Qy 1004 GCGCTCGCTTCTTCCACTTTGCTGCTGACCCCATCTCTATGCTTCTCTCGGGCCAA 1063
Db 952 GCGCTTAGCTTTCTTCCACTTTGCTGAAACCCCATCTCTATGCTTCTCTGGAGCCAA 1011
Qy 1064 GTTCAAAAGCTCTGCCAGCATGCACTCAACTCCATGAGCAGAGGCTCCAGCCTCAAGAT 1123
Db 1012 ATTAAACCTCTGCCAGCAGCATCTCCTCTGTGAGCAGAGGCTCCAGCCTCAAGAT 1071
Qy 1124 CTTTCCAAAGAAAGCGGGTGGACATCTTCCGTCTCCAGGAGTCAAGATCTCTCCAG 1183
Db 1072 CTTTCCAAAGAAAGCGAGTGGACATTCATCTGTTCCACTGAGTCTGAGTCTTCAAG 1131
Qy 1184 TTTTCACTCAGCTAACCTTTATGCAAGACTTATATAATATATATATATATATATAA 1243
Db 1132 TTTTCACTCAGCTAACACAGATGTAAAGACTTTTT-----TTTATACGATAATA 1183
Qy 1244 GAACCTTTTATGTTACACATTTTCCAGATATAAGAGACTGACAGCTTGTGACAGTTT 1303
Db 1184 ACTTTTATGTTACACATTTTTCAGATATAAAGACTGACCAATATTTGACAGTTT 1243
Qy 1304 TTTTATTTTAAATGACTGTGGAGTTTATGTTCTCTAGTTTGTGAGGTTTGAAT 1363
Db 1244 TATTGCTTGTGATTTTGT-----CTTGTGTTCTTTAGTTTGTGAGGTTTAAAT 1297
Qy 1364 TAAATTTATATAATATTTTGTGTTTGTTCATGTGAATGAGCGTCTAGGAGGACCT 1423

Db 1298 GACTTATTATATA-----TAAATTTTTTTTGTTCATATGATGTGTCTTAGGAGACCT 1353
Qy 1424 GTGGCCAAGTCTTTAGTAGCTGTTTATCTGTGTGTAGGACTGTAGAACTGTAGAGGAAGA 1483
Db 1354 GTGGCCAAGTCTTTAGTGTCTGTGTATGCTCGTGTAGGACTGTAGAA-----AAGGG 1405
Qy 1484 AACTGAACATTCAGAAATGTGTGTAATTAATTAAGCTAGCCGTGATCTCAGCTGTT 1543
Db 1406 AACTGAACATTCAGAGCGGTAGTGAATCACTGTAAGCTAGAAATGATCCCGAGCTGTT 1465
Qy 1544 GCTGCATA 1551
Db 1466 TATGCATA 1473

RESULT 15
US-10-342-887-912
; Sequence 912, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-198-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 912
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-342-887-912

Query Match 50.8%; Score 952.8; DB 7; Length 1679;
Best Local Similarity 80.2%; Pred. No. 2.8e-206;
Matches 1210; Conservative 0; Mismatches 252; Indels 46; Gaps 6;

Qy 44 GCAGGTGCAGGTAGCAGTGACCTCTGAGCGGTTTGGTGTCCGGTAAACACACCGCTG 103
Db 12 GCGGCAGCAGGTAGCAAGTAGCGCGAGGCGCTGAGTGTCTCCAGTAGCCCGCATCTG 71
Qy 104 TAGAGCGAGTGTGCCATGGACCGCATAGTGTGAGTATATACATCTCTGATAACTACTC 163
Db 72 GAGAACCGCGGTTACCATGGA-----GGGGATCAGTATATACATTCAGATAACTACAC 126
Qy 164 TGAAGAAGTGGGCTCTGGAGACTATGACTCCAAAGAAACCTCTCTCGGATGAAAA 223
Db 127 CGAGGAAATGGGCTCAGGGGACTATGACTCCATGAAGAAACCTCTCTCGTGAAGNAAA 186
Qy 224 CGTCCATTTCAATPAGGATCTTCTGCCCCACCATCTACTTCATCATCTTTCTTGTGCTGGCAT 283
Db 187 TGTAAATTTCAATAAAATCTTCTGCCCCACCATCTACTTCATCATCTTTCTTAACTGGCAT 246
Qy 284 AGTCGCAATGGATTTGGTGTATCTGTCATGGTTACCGAGAGAACTAAGGAGCATGAC 343
Db 247 TGTGGCAATGGATTTGGTGTATCTGTCATGGGTTACCGAGAGAAACTGAGAAAGCATGAC 306
Qy 344 GGACAAAGTACCGGCTGCACCTGTGAGTGGCTGACCTCTCTTTGTGTCATCACACTCCCTT 403
Db 307 GGACAAAGTACAGGCTGCACCTGTGAGTGGCGGACCTCTCTTTGTGTCATCACGCTTCCCTT 366

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1169.6	62.3	1651	7	US-11-136-527-2630	Sequence 2630, Appli
2	1074.4	57.2	1643	7	US-11-136-527-108	Sequence 108, Appli
3	960.4	51.2	1662	7	US-11-028-922A-3	Sequence 3, Appli
4	950.4	50.6	1400	7	US-11-136-527-6726	Sequence 6726, Appli
5	932.4	49.7	8747	6	US-10-955-054A-141	Sequence 141, Appli
6	905.6	48.2	1050	7	US-11-028-922A-4	Sequence 4, Appli
7	890.4	47.4	1400	7	US-11-136-527-4204	Sequence 4204, Appli
8	859	45.8	1225	6	US-10-955-054A-112	Sequence 112, Appli
9	808	43.0	1102	6	US-10-955-054A-121	Sequence 121, Appli
10	198.4	10.6	246960	7	US-11-121-086-8	Sequence 8, Appli
11	176.4	9.4	1680	7	US-11-136-527-153	Sequence 153, Appli
12	175	9.3	1324	7	US-11-136-527-2373	Sequence 2373, Appli
13	170	9.1	1433	6	US-10-750-185-54253	Sequence 54253, A
14	170	9.1	1433	6	US-10-750-623-54253	Sequence 54253, A
15	168.6	9.0	1400	7	US-11-136-527-4249	Sequence 4249, Appli
16	167.2	8.9	3062	6	US-10-995-561-120	Sequence 120, Appli
17	167.2	8.9	3100	6	US-10-775-169-254	Sequence 254, Appli
18	167.2	8.9	3101	6	US-10-995-561-119	Sequence 119, Appli
19	167.2	8.9	30151	6	US-10-995-561-13239	Sequence 13239, A
20	165.2	8.8	1348	7	US-11-136-527-3311	Sequence 3311, Appli
21	160.4	8.5	3177	7	US-11-127-877-25	Sequence 25, Appli
22	153	8.2	1960	7	US-11-136-527-617	Sequence 617, Appli
23	146.6	7.8	1059	7	US-11-068-686-19	Sequence 19, Appli

Db 302 TTGGGAAATTTTATGTAAGGCTGTGCATATCATCTACACCGCTCAACCTTTACAGCAGTG 361
 Qy 496 TTCTCATCTGGCTTCATCAGCCTGGAACGGTACCTCGCCATGTTCCAGCCACCAACA 555
 Db 362 TTCTCATCTGGCTTCATCAGCCTGGAACGGTACCTCGCCATGTTCCAGCCACCAACA 421
 Qy 556 GTCAAGGCCAAGGAACTGCTGGCTGAAAGGAGCTCTATGCGGCTCTGGATCCAG 615
 Db 422 GCAGAGCGGAGGAGCTGCTGGCTGAAAGGAGCTCTATGCGGCTCTGGATCCAG 481
 Qy 616 CCCTCTCTGACTATACCTGACTCTTCCTGCGACGCTCAGCCAGGGGACATCAGTC 675
 Db 482 CCCTCTCTGACTATACCTGACTCTTCCTGCGACGCTCAGCCAGGGGAC----- 534
 Qy 676 AGGGGATGACAGGTACATCTGACCGCTTTACCCCGATGACCTGTGGATGGTGT 735
 Db 535 -----GACAGGTACATCTGTGACCGCTTTACCCCGACAGCTGTGGATGGTGT 586
 Qy 736 TTCAATTCAGCATATAATGGTGGTCTCATCTGCGCGGACGCTCATCTCTCTCTGTT 795
 Db 587 TCAGTTTCAGCACATCATGGTGGTCTCATCTGCGGCGATCGTATCTCTCTCTGTT 646
 Qy 796 ACTGCATCATCATCTCTAAGCTGTCTACACTCCAAGGGCCACAGAGCGCAAGGCCCTCA 855
 Db 647 ACTGCATCATCATCTCCAAGCTGTCTACACTCCAAGGGCCACAGAGCGCAAGGCCCTCA 706
 Qy 856 AGACGACGATCATCTCATCTAGCTTTCTTTCCTGCTGGCTGCCATATATATGGGGA 915
 Db 707 AGACTACGGTTCATCTTCTGCTGCTTTCTTTCCTGCTGGCTGCCATATATATGGGGA 766
 Qy 916 TCAGCATCGACTCTCTCATCTTTTCGGAGTCAATCAAGCAAGGATGTGACTTCAGAGCA 975
 Db 767 TCAGCATCGACTCTCTCATCTTTTCGGAGTCAATCAAGCAAGGATGTGACTTCAGAGCG 826
 Qy 976 TTGTGCACAAAGTGGATCTCCATCAGAGAGCCCTCGCTTTCTTCCACTGTGTGCTGAACC 1035
 Db 827 TCGTGACACAGTGGATCTCCATCAGGAGGCCCTCGCTTTCTTCCACTGTGTGCTGAACC 886
 Qy 1036 CMATCTCTATGCTCTCTCGGGGCGAAGTTTCAAAAGCTCTGCCAGCATGCACTCACT 1095
 Db 887 CCATCTCTACGCTCTCTCGGGGCGAAGTTTCAAAAGCTCTGCCAGCATGCACTCACT 946
 Qy 1096 CCATGACGAGAGCTCCAGCTCAAGATCTTTTCCAAAGGAAAGCGGGTGGACCTCTT 1155
 Db 947 CCATGACGAGAGCTCCAGCTCAAGATCTTTTCCAAAGGAAAGCGGGTGGACCTCTT 1006
 Qy 1156 CGCTCTCCAGGAGTCAAGATCTCTCAGTTTTCACCTCCAGCTAACCTTATGCAAGACT 1215
 Db 1007 CGCTCTCCAGAGTCAAGATCTCTCAGTTTTCACCTCCAGCTAACCTTATGCAAGACT 1066
 Qy 1216 TATATAAT 1265
 Db 1067 TATATAAT 1126
 Qy 1266 TTCCAGATATAAGAGTCAAGCTCTGTGACAGTTTTCACCTCCAGCTAACCTTATGCAAGACT 1325
 Db 1127 TCCAGATATAAAGAGTCAAGCTCTGTGACAGTTTTCACCTCCAGCTAACCTTATGCAAGACT 1186
 Qy 1326 GCGAGTTTATGTTCCCTCT-----AGTTTTCGTGAGGTTTTCACCTTAAATTTATATAATA 1378
 Db 1187 TGTTTCTCAGTTTTCGTGAGGTTTTCACCTTAAATTTATATAATA 1246
 Qy 1379 T-----TGTTTTCGTGAGGTTTTCACCTTAAATTTATATAATA 1427
 Db 1247 TTGGTTTTTTCGTGAGGTTTTCACCTTAAATTTATATAATA 1306
 Qy 1428 CCAAGTTCTTAGTACGTTTTCGTGAGGTTTTCACCTTAAATTTATATAATA 1487
 Db 1307 CCAAGTTCTTAGTACGTTTTCGTGAGGTTTTCACCTTAAATTTATATAATA 1366
 Qy 1488 GAAACATTCAGAAATGTGTGTAATTTGAATTAAGCTAGCCGTGATCTCTCAGCTGTGCTG 1547

Db 1367 GAACGCTCCAGAAATGTGTGTAATAAGCTAGAAAGTGAACCT-AGCTGTGCTG 1425
 Qy 1548 CATATCTCTTCATTCGAGGAGCAGCCACCCACCCACCCACCCACCCACCCACCCATCTTAA 1607
 Db 1426 CATATCTCTT-----CGCCCGCCACCCCGTTCCTGA 1459
 Qy 1608 ATTGTTTGGTATGCTGTGTGATGGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1667
 Db 1460 ATTGTTTGGTGTGCTGTG----- 1480
 Qy 1668 TTTTCTCTTAAAGATGGCACTTAAACCAAGCCTGAATGGGTAGAAATGCTGG 1727
 Db 1481 GTTCTCTCTAGAAATGGCACTTAAACCAAGCCTGAATGGT-ATAGAAATGCTGG- 1538
 Qy 1728 GTTCTCTCTAGAAATGGCACTTAAACCAAGCCTGAATGGT-ATAGAAATGCTGG- 1787
 Db 1539 -----GTTTTTCTTCAGTTTTCAGGGTGGATGATTTTCAGTACCTACAA 1585
 Qy 1788 ATGTACAGTCTTGTATATACATTTTAATAAAGTCAATGATAAATTAATAAATAAATA 1847
 Db 1586 ATGTACAGTCTTGTATATATATGTTTAATAAAGTCAATGATAAATTAATAAATAAATA 1645
 Qy 1848 AAAAAA 1853
 Db 1646 AAAAAA 1651
 RESULT 2
 US-11-136-527-108
 ; Sequence 108, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 108
 ; LENGTH: 1643
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-11-136-527-108
 Query Match 57.2%; Score 1074.4; DB 7; Length 1643;
 Best Local Similarity 80.4%; Pred. No. 3.6e-197;
 Matches 1448; Conservative 20; Mismatches 146; Indels 188; Gaps 11;
 Qy 79 GGTGCTCCGGTAAACCAACCGCTGTAGAGCGAGTGTGGCATGGAACCGATCAGTGTGA 138
 Db 3 GGTGCTCCGGTGTAGTACCAGGGCTGGAGCGAGCATTCGCCATGGAA----- 49
 Qy 139 GTATATACACTTCTGTATAACTCTCTGAAGAAGTGGGGTCTGGAGACTATGACTCCAACA 198
 Db 50 --ATATACACTTTCGGATAACTCTCGAAGAAGTAGGGTCTGGAGACTATGACTCCAACA 107
 Qy 199 AGGAACCTGCTTTCGGGATGAACCGTCCATTTCAATAGGATCTTCTGCCACCATCT 258
 Db 108 AGGAACCTGCTTTCGGGATGAACCGAATACTTCAACAGGATCTTCTGCCACCATCT 167
 Qy 259 ACTTCATCATCTTCTGACTGGCATAGTGGCAATGGATGGTGGTGGTGGTGGTGGTGGTGGT 318
 Db 168 ATTTATCATCTTCTGACTGGCATAGTGGGCAATGGTGGTGGTGGTGGTGGTGGTGGTGGT 227
 Qy 319 ACCAGAAGAAGCTTAAGGAGCATGACGAGCAAGTACCGGCTGACCTGTGAGTGGCTGACC 378
 Db 228 ACCAGAAGAAGCTGAGGAGCATGACGAGCAAGTACCGGCTGACCTGTGAGTGGCTGACC 287
 Qy 379 TCCTCTTGTTCATCACACTCCCTTCTGGGAGTTGATGCCATGGCTGACTGTTG 438

[illegible][illegible]

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RESULT 3
US-11-028-922A-3
; Sequence 3, Application US/11028922A
; Publication No. US20050271639A1
; GENERAL INFORMATION:
; APPLICANT: Perrin, Marc
; TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
; FILE REFERENCE: CCF-7019
; CURRENT APPLICATION NUMBER: US/11/028,922A
; CURRENT FILING DATE: 2005-01-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-028-922A-3

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	Query Match	51.2%;	Score 960.4;	DB 7;	Length 1662;
	Best Local Similarity	76.3%;	Pred. No. 2.7e-175;		
	Matches 1371;	Conservative	0;	Mismatches 291;	Indels 136; Gaps 10;
Qy	68	CTGAGGCGTTTGGTCTCCGGTAACCAACGCGCTGTAGAGCGAGTGTTCCTATGGAAACC	127		
Db	1	CCGAGGCGCTTGAGTGTCCAGTAGCCACCGCATCTCGAGAAACCAAGCGGTTTACCATGGA--	58		
Qy	128	GATCAGTGTCAGATATATACACTTCTGATTACTACTCTGAAGAAAGTGGGTCCTGGAGACTA	187		
Db	59	---GGGATCAGTATATATACACTTTCAGATACTACACCGAGGAAATGGCTCAGGGGACTA	115		
Qy	188	TGACTCCAAAGGAACCCCTGCTTCGGGATGAAACGTCCTATTCATAGGATCTTCCT	247		
Db	116	TGACTCCATGAGGAACCCCTGTTTCGGTGAAGAAATGCTAAATTCATAAATCTTCCT	175		
Qy	248	GCCACCATCTACTTCATCATCTTCTTGACTGCGATAGTCGGCAATGGATGTGTGATCTCT	307		
Db	176	GCCACCATCTACTCCATCATCTTCTTAACTGGCATTTGTGGCAATGGAATGGTCACTCT	235		
Qy	308	GGTATGGGTTTACAGAAGAAGCTAAGGACATGACGGACAAGTACCGGCTGCACCTGTC	367		
Db	236	GGTCATGGGTTTACAGAAGAAATCTGAGAAGCATGACGGAACAGTACAGGCTGCACCTGTC	295		

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QY 368 AGTGGCTGACCTCTCTTTGTCATCACACTCCCTCTGGGCGAGTTGATGCCATGGCTGA 427
Db |||||
QY 296 AGTGGCGAGCTCTCTTTGTCATCACGCTTCCCTCTGGGCGAGTTGATGCCATGGCAA 355
Db |||||
QY 428 CTGGTACTTTGGGAAATTTTGTGAAGGCTGTCATATCATCTACATCTGTCACACCTCTA 487
Db |||||
QY 356 CTGGTACTTTGGGAACTTCCTATGCAAGGCGAGTCCATGTCTATACACAGTCAACCTCTA 415
QY 488 CAGCAGGTTCTCATCTGCGCTTCTATCAGCCTGGACCGGTACTGCGCATTTGTCACGC 547
Db |||||
QY 416 CAGCAGTGTCTCATCTGCGCTTCTATCAGTCTGGACCGGTACTGCGCATGCTCCACGC 475
QY 548 CACCAACAGTCAAGGCCAAGGAACTGCTGGCTGAAAGGCGAGTCTATGCTGGCGCTCTG 607
Db |||||
QY 476 CACCAACAGTCAAGGCCAAGGAGCTGTTGGCTGAAAGGTGCTATGTTGGCGTCTG 535
QY 608 GATCCAGGCCCTCTCTGACTATACCTGACTTTCATCTTTGCCGAGCTCAGCCAGGGGA 667
Db |||||
QY 536 GATCCCTGCGCTCTCTGCTGACTATTCGCGACTTTCATCTTTGCCAAG- 582
QY 668 CATCAGTCAGGGGATGACAGGTACATCTGTGACCGCTTACCCGATAGCTGTGGAT 727
Db |||||
QY 583 --TCAGTGGGCGAGTACAGATATATCTGTGACCGCTTACCCCAATGACTTGTGGGT 640
QY 728 GGTGGTGTTCAAATTCAGCATATAATGGTGGGTCTCATCTGCCGGCATCGTCATCT 787
Db |||||
QY 641 GGTGTGTTCCAGTTTCAGCACATCATGGTTGGCTTATCTGCTGTGTTATGTCATCT 700
QY 788 CTCCTGTACTGCATCATCTCTAAGCTGTCCACTCCAAAGGGCCACAGAGCGCAA 847
Db |||||
QY 701 GTCCTGTATTGCTATTCATCTCCAGCTGTCCACTCCAAAGGGCCACAGAGCGCAA 760
QY 848 GGCCTCTCAAGACACAGTCTATCTCATCTCTTCTTTGCGCTGCTGGTGCATATTA 907
Db |||||
QY 761 GGCCTCTCAAGACACAGTCTATCTCATCTCTGGCTTCTTCCGCTGTGGTGCCTACTA 820
QY 908 TGTGGGATCAGATCAGCTCTCTTCTATCTTTGGGAGTCTCAAGCAAGGATGCTACTT 967
Db |||||
QY 821 CATTTGGATCAGATCAGCTCTCTTCTATCTCTCTGGAATCATCAAGCAAGGATGCTACTT 880
QY 968 CGAGAGCATTTGTCCACAAGTGGATCTCCATCACAGAGGCCCTCGCCTTCTTCCACTGTTG 1027
Db |||||
QY 881 TGAGAACACTGTGCACAAGTGGATTTCCATCACGAGGCCCTAGCTTCTTCCACTGTTG 940
QY 1028 CTTGAACCCCATCTCTATGCTTCTCTGGGGCGAAGTTCAAAGCTCTGCCCAGCATGC 1087
Db |||||
QY 941 TCTGAACCCCATCTCTATGCTTCTCTTGGAGCCAAATTTAAACCTCTGCCCAGCACGC 1000
QY 1088 ACTCAATCCATGACGAGAGGCTCCAGCTCAAGATCCTTTCCAAAGGAAGCGGGTGG 1147
Db |||||
QY 1001 ACTCAGCTCTGTGAGCAGAGGGTCCAGCTCAAGATCCTCTCCAAAGGAAGCGAGTGG 1060
QY 1148 ACACCTCTTCGCTCCACGAGTCAGAAATCCTCAGTTTTTCACTCCAGCTAACCCCTTATG 1207
Db |||||
QY 1061 ACATTTCATCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTTCACTCCAGCTAA- 1112
QY 1208 CAAAGACTTATATATATATATATATATATATATATATATATATATATATATATATATAT 1267
Db |||||
QY 1113 CACAGATGTAAGAGACTTTTTTTTTTATACGATAAATAAATTAATTAAGTTTACACATTTT 1172
QY 1268 CCAGATATAGAGACTGACAGCTCTGTACAGTTTTTTTTTTTTTTTTTTTTTAAATTGACTGTGG 1327
Db |||||
QY 1173 TCAGATATATAAGACTGACCAATATGTACAGTTTTTATTTGCTGTGGATTTTGT- 1229
QY 1328 GAGTTTATGTTCTCTAGTTTTTGTGAGGTTTGACTTTTAAATTTATATAAATAATTTGTTTTT 1387
Db |||||
QY 1230 ---CTTGTGTTCTTTAGTTTTTGTGAAGTTTAATGACTTATTTATA----TAAATTTT 1282
QY 1388 GTTTGTTTATGATGATGACGCTTAGGAGGAGGCTGTGGCCAAAGTTCTTAGTAGCTGTT 1447
Db |||||
QY 1283 TTTTGTGTTTATATGATGTGTGTCTAGGCGAGGCTGTGGCCAAAGTTCTTAGTTGCTGTA 1342
QY 1448 TATCTGTGTAGGACTGTAGAACTGTAGAGGAAGAACTGAACATTTCCAGAAATGTGTGG 1507
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Db 1343 TGCTCTGCTGGTAGGACTGTAGAA-----AAGGGAACCTGAACATTTCCAGAGCGTGTAG 1394
QY 1508 TAAATGGAATAAAGCTAGCGGTGATCTCAGCTGTTGCTGTCATATCTCTTCAATCCGAG 1567
Db |||||
QY 1395 TGAATCACGTAAGCTAGAAATGATCCCGAGCTGTTTATGTCATAGATAATCTCTCCA--- 1451
QY 1568 GAGCACCCACCCACCCACCCACCCACCCCACTTCTTAAATTTGTTGTTATGCTGTGT 1627
Db 1452 ----- 1451
QY 1628 GATGGTTTGTGTTGTTTGTGTTGTTGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 1687
Db 1452 -----TTCCGCTGGAACGTTTTTCCGTGTTCTTAAGACGTGATTTTGCCTGTAAGAGTGC 1506
QY 1688 ACTTAAACCAAGCCCTGAAATGGTGGTGAAGAAATGCTGGGGTTTTTTTTTGTGTTGTTGTT 1747
Db 1507 ACTTAAACCAAGCCCAAGTGGT-ATAGAAATGCTGG-----T 1545
QY 1748 TTTTCAGTTTTCAAGAGTAGATTGACTTCAGTCCCTTACAAATGTACAGTCTTGTATTACA 1807
Db 1546 TTTTCAGTTTTCAGGAGTGGGTTGATTTTCCAGCACCTAC-AGTGTACAGTCTTGTATTAG 1604
QY 1808 TTGTTAATAAAGTCAATGATAACTTAAATAAATAAATAAATAAATAAATAAATAAATAA 1865
Db 1605 TTGTTAATAAAGTACATGTTAACTTAAATAAATAAATAAATAAATAAATAAATAAATAA 1662
```

RESULT 4
US-11-136-527-6726
; Sequence 6726, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6726
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6726

Query Match 50.6%; Score 950; DB 7; Length 1400;
Best Local Similarity 82.8%; Pred. No. 2,5e-173;
Matches 1239; Conservative 4; Mismatches 129; Indels 124; Gaps 9;

QY 386 TGTATCATCACATCCCTCTCTGGGCGAGTTGATGCCATGGCTGACTGTTGGGAAAT 445
Db 1 TGTATCATCACATCCCTCTCTGGGCGAGTGGACGCCATGGCTGACTGTTGGGAAAT 60

QY 446 TTTGTGTAAGGCTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCGTTCTCATCT 505
Db 61 TTTATGTAAGGCTGTGCATATCATCTACACCGTCAACCTTTTACAGCAGTGTCTCATCT 120

QY 506 GGCCTTTTCATCAGCTGGACCGGTACTCTGCCATTGTCCACGCCACCACACAGTCAAAAGGC 565
Db 121 GGCCTTTTCATCAGCTGGACCGGTACTCTGCCATTGTCCACGCCACCACACAGCAGCGC 180

QY 566 AAGGAACTGCTGGCTGAAAAGCGCAGTCTATGTGGCGCTCTGATCCAGCCCTCTCTCT 625
Db 181 GAGGAAGCTGCTGGCTGAAAAGCGCGTCTATGTGGGTGTCTGATCCCGCCCTCTCTCT 240

QY 626 GACTATACCTGACTTCATCTTTGCCGAGCTCAGCCAGGGGACATCAGTCAGGGGATGA 685
Db 241 GACTATCTGTGATCATCTTCCGCGATGTCCGCGAGGGGAC-----GG 285


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QY 586 CAGGTACATCTGTGACCGCCTTTACCCCGATAGCCTGTGTGATGGTGTGTTCAATTCCA 745
Db 286 CAGGTACATCTGTGACCGCCTTTACCCCGACAGCCTGTGTGATGGTGTGTTCCAGTTCCA 345
QY 746 GCATATAATGGTGGGTCTCATCTCTGCCCGGCATCGTCATCTCTCTCTGTGTACTGTCATCAT 805
Db 346 GCATATCATGGTGGGTCTCATCTCTGCCCGGCATCGTCATCTCTCTCTGTGTACTGTCATCAT 405
QY 806 CATCTCTAAGCTGTACATCTCCAAAGGGCCACCAAGAGCGCAAGGCCCTCAAGACGACAGT 865
Db 406 CATCTCAAGCTGTACATCTCCAAAGGGCCACCAAGAGCGCAAGGCCCTCAAGACTACGGT 465
QY 866 CATCTCATCTAGCTTTCTTTGGCTGCTGGCTGCCATATATGTGGGGATCAGCATCGA 925
Db 466 CATCTCTATCTGGCTTTCTTTGGCTGCTGGCTGCCATATATGTGGGGATCAGCATCGA 525
QY 926 CTCTCTCATCTTTGGGAGTCATCAAGCAAGATGTGACTTCGAGAGCATGTGCACAA 985
Db 526 TTCTCTCATCTTTGGAGGTCAATCAAGCAAGATGTGAGTTTGAGAGCGCTGTGCACRA 585
QY 986 GTGGATCTCCATCAGAGGCCCTCGCTTTCTTCCACTGTGTGCTGAAACCCCATCTCTTA 1045
Db 586 GTGGATCTCCATCAGAGGCCCTCGCTTTCTTCCACTGTGTGCTGAAACCCCATCTCTTA 645
QY 1046 TGGCTTCTCGGGCCCAAGTTCAAAAGCTCTGCGCAGCATGCACTCACTCCATGAGCAG 1105
Db 646 CGCTTCTCGGGCCCAAAATTCAGAGCTCTCGGCGAGCATGCACTCAATTCATGAGCAG 705
QY 1106 AGCTCCAGCTCAAGATCTTTCCAAAGGAAGCGGGTGGACACTCTTCGCTCTCCAC 1165
Db 706 AGCTCCAGCTCAAGATCTTTCCAAAGGAAGCGGGTGGACACTCTTCGCTCTCCAC 765
QY 1166 GGAGTCAGAAATCTCCAGTTTTCACCTCAGCTAACCTTTATGCAAGACTTATATAATAT 1225
Db 766 AGAGTCAGAAATCTCCAGTTTTCACCTCAGCTAACCTTTAGCAAGACATATATAATAT 825
QY 1226 ATATATATATAT-----GATAAAGAACTTTTATATGTTTACATTTTCCAGATAT 1275
Db 826 ATATATATATATATATATGACAAAGAACTTTTATATGTTTATGTTTACATTTCCAGATAT 885
QY 1276 AAGAGCTGACCACTGTGTGACAGTTTATATGTTTATATGTTTATGTTTATGTTTATGTTTAT 1335
Db 886 AAGAGCTGACCACTGTGTGACAGTTTATATGTTTATATGTTTATGTTTATGTTTATGTTTATGTTTAT 945
QY 1336 GTTCTCTCT-----AGTTTGTGAGTTTGTGCTTAATTTATATAATAT----- 1379
Db 946 GTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1005
QY 1380 --TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1437
Db 1006 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1065
QY 1438 AGTAGCTGTTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1497
Db 1066 AGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1125
QY 1498 GAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1557
Db 1126 GAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1184
QY 1558 TCATTCGAGGAGCAGCCCCACCCCCACCCCCACCCCCACCCCCACCCCCACCCCCACCCCCACCCCC 1617
Db 1185 T-----CGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCC 1218
QY 1618 TATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1677
Db 1219 TGTGTGTGTGT-----GTTTCTCTGT 1239
QY 1678 AAAAGATGGCACTTAAACCAAAAGCCTGAAATGGTGTGAGAAATGCTGGGGTGTGTGTGTGTGTGTGTGT 1737
Db 1240 AGAAGATGGCACTTAAACCAAAAGCCTGAAATGGT-ATAGAAATGCTGG----- 1287
QY 1738 TTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1797
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RESULT 5

```
US-10-955-054A-141
; Sequence 141, Application US/10955054A
; Publication No. US20050266420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AYERS, MARK
; APPLICANT: SPEC, JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTXC:880US
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
; LENGTH: 8747
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-141
```

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Query Match 49.7%; Score 932.4; DB 6; Length 8747;
Best Local Similarity 81.5%; Pred. No. 1e-169;
Matches 1156; Conservative 0; Mismatches 221; Indels 41; Gaps 5;

QY 134 TGTGAGTATATACACTCTCTGATAACTACTCTGAAGAAGTGGGTCTGGAGACTATGACTC 193
Db 4861 TTTGCAGATATACACTTTCAGATAACTACACCGAGGAATGGGCTCAGGGGACTATGACTC 4920
QY 194 CAACAAGGAACCTCTCTCGGATGAAACGTCCTCAATAGGATCTTCTGCCCCAC 253
Db 4921 CATGAAGGAACCTCTCTCGTGAAGAAATGCTAATTTCAATAAATCTTCTGCCCCAC 4980
QY 254 CATCTACTTCACTCTCTTGTAGCTGGCATAGTGGCAATGGATTTGGTATCTCTGTCTCAT 313
Db 4981 CATCTACTTCACTCTCTTAACTGGCATTTGGGCAATGGATTTGGTATCTCTGTCTCAT 5040
QY 314 GGGTTACCAAGAACTAGAGGAGCATGACGGAAGTACCGGCTGCACCTGTCTGAGTGGC 373
Db 5041 GGGTTACCAAGAACTAGAGAGCATGACGGAAGTACAGGCTGCACCTGTCTGAGTGGC 5100
QY 374 TGACCTCTCTTTGTCTATCACACTCCCTCTTCTGGGCGAGTTGATGSCCATGGCTGACTGGTA 433
Db 5101 CGACCTCTCTTTGTCTATCAGGCTTCCCTTCTGGGCGAGTTGATGSCCATGGTA 5160
QY 434 CTTTGGGAAATTTTGTGTGAAGCTGTCCATATCATCTACATGTCAACCTCTACAGCAG 493
Db 5161 CTTTGGGAACTTCTTATGCAAGGCACTCCATGTCTATTACACAGTCAACCTCTACAGCAG 5220
QY 494 CGTTCTCATCTTGGCCCTTCAATCAGCTGGACCGGTACCTCGCCATGTCCACGCCACCAA 553
Db 5221 TGTCTCATCTTGGCCCTTCAATCAGCTGGACCGGTACCTCGCCATGTCCACGCCACCAA 5280
QY 554 CAGTCAAGGCCCAAGGAACTGCTGGCTGAAAGGAGTCTATGTGGGCGCTCTGGATCCC 613
Db 5281 CAGTCAAGGCCCAAGGAGCTGTTGCTGAAAGGAGTCTATGTGGGCGCTCTGGATCCC 5340
QY 614 AGCCCTCTCTGACTATACCTGACTTTCATCTTTTGGCGAGCTCAGCCAGGGGAGCATCAG 673
Db 5341 TGGCCCTCTCTGACTATTTCCCGACTTTCATCTTTTGGCAACG-----TCAG 5385
QY 674 TCAGGGGAGTACAGCTACATCTGTACCGCCCTTTTACCCCGATAGCTGTGGATGGTGT 733
Db 5386 TGAGGCGAGTACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGTGTGT 5445
```

734 GTTTCATATCCAGCATATATGTTGGTCTCATCTCGCCGGCATCGTCACTCTCTCTG 793
|||
Db 5446 GTTCCAGTTTCAGACATCATGTTGGCTTATCTGCTGTTATGTTGTCATCTCTCTG 5505
|||
Qy 794 TTACTGCATCATCTCTTAAGCTGTACACCTCAAGGGCCACAGAGCGCAAGCCCT 853
|||
Db 5506 CTATTGCATTATCATCTCAAGCTGTACACCTCAAGGGCCACAGAGCGCAAGCCCT 5565
|||
Qy 854 CAAGACGACAGTCACTCTCATCTAGTCTTCTTGGCTGTGCTGCTGCCATATTATGGG 913
|||
Db 5566 CAAGACGACAGTCACTCTCATCTAGTCTTCTTGGCTGTGCTGCTGCCATATTATGG 5625
|||
Qy 914 GATCAGCATCGACTCTCTCATCTCTTGGAGTCACTCAAGCAAGGATGTGACTTTCAGAG 973
|||
Db 5626 GATCAGCATCGACTCTCTCATCTCTTGGAGTCACTCAAGCAAGGATGTGACTTTCAGAA 5685
|||
Qy 974 CATTTGCAACAGTGGATCTCCATCAAGAGGCTCTGCTTCTTCCACTTTGCTCGAA 1033
|||
Db 5686 CACTGTGCAACAGTGGATTTCCATCAAGAGGCTCTGCTTCTTCCACTTTGCTCGAA 5745
|||
Qy 1034 CCCCATCTCTATGCTCTCTCGGGCCAGTTCAAGAGTCTGCCCAGCATGCACTCAA 1093
|||
Db 5746 CCCCATCTCTATGCTCTCTCGGGCCAGTTCAAGAGTCTGCCCAGCATGCACTCAA 5805
|||
Qy 1094 CTCATGAGCAGAGGCTCCAGCTCAAGATCTCTTCCAAAGGAAAGCGGGTGGACATC 1153
|||
Db 5806 CTCGTGAGCAGAGGCTCCAGCTCAAGATCTCTTCCAAAGGAAAGCGGGTGGACATC 5865
|||
Qy 1154 TTCCTGTCTCAGAGGTCAGAACTCTCAGATTTTCACTCAGCTAACCTTTATGCAAGA 1213
|||
Db 5866 ATCTGTTTCCACTGAGTCTGAGTCTTCAAGTCTTCACTCCAGCTAA-----CACAGA 5917
|||
Qy 1214 CTTAT 1273
|||
Db 5918 TGTAAAGAGCTTTTAT 5977
|||
Qy 1274 ATAAGAGACTGACAGTCTTGTACAGTTTATATATATATATATATATATATATATATAT 1333
|||
Db 5978 ATAAAGACTGACCAAT 6031
|||
Qy 1334 ATGTTCTCTAGTTTTGTGAGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 1393
|||
Db 6032 GTGTTCTTTAGTTTTGTGAGTTTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 6087
|||
Qy 1394 TTCAATGATGAGCTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1453
|||
Db 6088 TTCAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6147
|||
Qy 1454 TGTGTAGGAGCTGTAGAACTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1513
|||
Db 6148 GTGTTAGGAGCTGTAGAA-----AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6199
|||
Qy 1514 GAATAAGCTAGCGGTGATCCTCAGCTGTTGCTGCATA 1551
|||
Db 6200 ACGTAAAGCTAGAAATGATCCCCAGCTGTTTATGCATA 6237
|||

RESULT 6

US-11-028-922A-4
; Sequence 4, Application US/11028922A
; Publication No. US20050271639A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Marc
; TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
; FILE REFERENCE: CCF-7019
; CURRENT APPLICATION NUMBER: US/11/028,922A
; CURRENT FILING DATE: 2005-01-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1050
; TYPE: DNA

i ORGANISM: Rattus norvegicus
US-11-028-922A-4
Query Match 48.2%; Score 905.6; DB 7; Length 1050;
Best Local Similarity 91.6%; Pred. No. 7.5e-165;
Matches 975; Conservative 0; Mismatches 74; Indels 15; Gaps 1;
Qy 136 TGAGTATATACACTTCTGTATAACTACTCTGAAAGAGTGGGCTCTGGAGACTATGACTCCA 195
|||
Db 2 TGGAAATATACACTTTCGGATACTACTCCGAAGAGTAGGGTCTGGAGACTATGACTCCA 61
|||
Qy 196 ACAAGAAACCTTCTCGGGATGAAACGTCCATTTCAATAGGATCTTCTTCCGCCACCA 255
|||
Db 62 ACAAGAAACCTTCTCGGGATGAAACGTCCATTTCAATAGGATCTTCTTCCGCCACCA 121
|||
Qy 256 TCTACTTCATCATCTTCTGACTGGCATAGTCGGCAATGGAATTTGGTGTATCTTGGTCATCG 315
|||
Db 122 TCTATTTTATCATCTTCTGACTGGCATAGTGGGCAATGGGTTGGTAATCTTGGTCATGG 181
|||
Qy 316 GTTACCAGAAAGCTTAAGGAGCATGACGGAACAAGTACCGGCTGCACCTGTGAGTGGCTG 375
|||
Db 182 GTTACCAGAAAGCTGAGGAGCATGACAGACAAGTACCGGCTGCACCTGTGCGTGGCTG 241
|||
Qy 376 ACTCTCTTTTGTCTATFACACTCCCTTCTGGGAGTTGATGCCATGGCTGACTGTACT 435
|||
Db 242 ACTCTCTTTTGTCTATFACACTCCCTTCTGGGAGTGGACGCCATGGCTGACTGTACT 301
|||
Qy 436 TTGGGAAATTTTGTCTAAGGCTGCCATATCATCTACACTGTCAACCTCTACAGCAGCG 495
|||
Db 302 TTGGGAAATTTTGTCTAAGGCTGCCATATCATCTACACCCTCAACCTTTACAGCAGTG 361
|||
Qy 496 TTCTCATCTCGGCTTTCATCAGCCTGGACCGGTACCTCGCCATTTGTCCACGCCACCAACA 555
|||
Db 362 TTCTCATCTCGGCTTTCATCAGCCTGGACCGGTACCTCGCCATTTGTCCACGCCACCAACA 421
|||
Qy 556 GTCAAAGCCAAAGGAAACTGTGGTGTGAAAGGAGTCTATGTGGGCTGTGATGCCAG 615
|||
Db 422 GCCAGAGCGGAGGAGTGTGGTGTGAAAGGCGCTCTATGTGGGCTGTGATGCCAG 481
|||
Qy 616 CCTCTCTCTGACTATACCTGACTTTCATCTTCCGAGCTGAGCCAGCGGAGGAGGAGGAGG 675
|||
Db 482 CCTCTCTCTGACTATCTCAAGCTGTACATCTTCCGAGCTGAGCCAGGAGGAGGAGGAGG 534
|||
Qy 676 AGGGGAGTACAGAGTACATCTGTGACCGCTTTACCCGATAGCCTGTGGATGGTGTGT 735
|||
Db 535 -----GGCAGGTACATCTGTGACCGCTTTACCCGACAGCCTGTGATGGTGTGT 586
|||
Qy 736 TTCAATTCAGCATATATATGTTGGTCTCATCTTGGCCCGGATCTGTCATCTCTCTGT 795
|||
Db 587 TCAGTTTCAGCAGCATCATGTTGGTCTCATCTTCCGCGGCTACGTCATCTCTCTGT 646
|||
Qy 796 ACTGCATCATCTCTTAAGCTGTACACTCCAAAGGCGCACAGAGCGCAAGGCGGCTCA 855
|||
Db 647 ACTGCATCATCTCTCAAGCTGTACACTCCAAAGGCGCACAGAGCGGAGGCGGCTCA 706
|||
Qy 856 AGACGACAGTCACTCTCATCTTAGCTTTCTTTCCTGTGGCTGCGCATATTATGTGGGA 915
|||
Db 707 AGACTACGCTCATCTTATCTTGGCTTTCTTTCCTGTGGCTTACCGTATTACGTGGGA 766
|||
Qy 916 TCAGCATCGACTCTCTTTCATCTTGGGAGTCACTCAAGCAAGATGTGACTTTCGAGAGCA 975
|||
Db 767 TCAGCATCGATTCTCTTTCATCTTGGGAGTCACTCAAGCAAGATGTGACTTTCGAGAGCG 826
|||
Qy 976 TTGTGCACAAGTGGATCTCCATCAGAGGCGCTCGCCCTTCTTCCACTGTGTGCTGAACC 1035
|||
Db 827 TGTGCAACAAGTGGATCTCCATCAGCGAGGCGCTCGCCCTTCTTCCACTGTGTGCTGAACC 886
|||
Qy 1036 CCATCTCTATGCTTCTCTCGGGCGCAAGTCTCAAAAGCTCTGCCAGCATGCACTCAACT 1095
|||
Db 887 CCATCTCTATGCTTCTCTCGGGCGCAAAATTCAAGAGCTCCGCGCAGCATGCACTCAATT 946
|||
Qy 1096 CCATGAGCAGGCTCCAGCTTCAAGATCTTTCAAAGAGGAGCGGGGTGGACATCTTT 1155
|||


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Db 294 ACCTCCTCTTGTTCATCAGCGCTCCCTCTTGGGAGTTGATCCGCTGGCAAACTGGTACT 353
Qy 436 TTGGGAAATTTTGTGTAAAGCTGTTCATATCATCTACATCTGTCACCTCTACAGAGCG 495
Db 354 TTGGGAAATTTTGTGTAAAGCTGTTCATATCATCTACATCTGTCACCTCTACAGAGCG 413
Qy 496 TTCTCATCTGGGCTTCATCAGCGCTGACCGGTGACCTGCGCATTTGTCACGCCAACAA 555
Db 414 TCCTCATCTGGGCTTCATCAGCTGACCGGTGACCTGCGCATTTGTCACGCCAACAA 473
Qy 556 GTCAAGGCCAAGGAAATCTGTGGCTGAAAGGAGCTCTATGTGGGGCTGTGGATCCAG 615
Db 474 GTCAAGGCCAAGGAAATCTGTGGCTGAAAGGAGCTCTATGTGGGGCTGTGGATCCAG 533
Qy 616 CCCTCCTCTGATATATACCTGATCTTATCTTTGCGGAGCTGACGAGGGGGAACATGATC 675
Db 534 CCCTCCTCTGATATATACCTGATCTTATCTTTGCGGAGCTGACGAGGGGGAACATGATC 578
Qy 676 AGGGGATGACAGGTATATCTGTGACCGCTTTTACCCGATAGCTGTGGATGGTGT 735
Db 579 AGGGGATGACAGGTATATCTGTGACCGCTTTTACCCGATAGCTGTGGATGGTGT 638
Qy 736 TTCAATTTCCAGCATATATATGTTGGGTCTCATCTGCGCGCATCGTCTCTCTCTGTT 795
Db 639 TCCAGTTTCCAGCATATATGTTGGGTCTCATCTGCGCGCATCGTCTCTCTCTGTT 698
Qy 796 ACTGATCATCATCTTAAAGTGTGACACTCAAGGAGGACCAAGAGCGGAGGAGGAGGAGG 855
Db 699 ATTGCATTATCATCTCAAGCTGTGACACTCAAGGAGGACCAAGAGCGGAGGAGGAGGAGG 758
Qy 856 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 915
Db 759 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 818
Qy 916 TCAGCATGAGTCTCTTTCATCTTTTGGGAGTCTCAAGCAAGGAGGAGGAGGAGGAGGAGG 975
Db 819 TCAGCATGAGTCTCTTTCATCTTTTGGGAGTCTCAAGCAAGGAGGAGGAGGAGGAGGAGG 878
Qy 976 TTGTGCAAGAGTGTGATCTCATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1035
Db 879 CTGTGCAAGAGTGTGATCTCATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 938
Qy 1036 CCATCCTCTATGCTTCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1095
Db 939 CCATCCTCTATGCTTCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 998
Qy 1096 CCATGAGCAGAGGCTCCAGCTCAAGATCTTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAG 1155
Db 999 CTGTGAGCAGAGGCTCCAGCTCAAGATCTTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1058
Qy 1156 CCCTCTCCAGGAGTCAAGATCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1199
Db 1059 CTGTGTTCCAGTCTGAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCT 1102

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RESULT 10
US-11-121-086-8
; Sequence 8, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-0000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 246960
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-11-121-086-8
Query Match 10.4%; Score 198.4; DB 7; Length 246960;
Best Local Similarity 53.8%; Pred. No. 1.7e-28;
Matches 456; Conservative 0; Mismatches 386; Indels 6; Gaps 2;

Qy 231 TTCAATAGATCTTCTGCCCCACCATCTACTTTCATCATCTTCTTGTAGTGGCATAGTGGC 290
Db 120644 TTCAAGGCGGTGTTCGTGCCCCGGGCTACAGGCTCATCTTCTCTGCGCGTATCGGC 120703
Qy 291 AATGGATTTGTGTGATCTCTGGTTCATGGGTTTACAGAGAAGCTAAGGAGCATGACGGACA 350
Db 120704 AAGTCTCTGTGTGTGTGATCTCTGGAGCGGACCGGAGACAGCAGTTCACGGAGACC 120763
Qy 351 TACCGGCTGCACCTGTCTAGTGGCTGACCTCTCTTTTGTATCATCATCTCCCTTTCTGGGCA 410
Db 120764 TTCTGTTCACCTGTGCGGTGGCGACCTCTCTGCTGTCTTCTTGTCCCTTTGGCGTG 120823
Qy 411 GTTGATGCCATGGCTGACCTGTGTTGGGAAATTTTGTGTAAAGGCTGTCCATATCATC 470
Db 120824 GCCGAGGGCTCTGTGGGCTGGGTCCTGGGAGACCTTCTCTGCAAAACTGTGATTGCCCTG 120883
Qy 471 TACACTGTCAACCTCTACAGCAGCGTTCCTCATCTGSCCTTTCATCAGCCTGGACCGGTAC 530
Db 120884 CACAAAGTCAACTTCTACTGACGACGCTGCTCTGCGCTGCAATGCCGTGGACCGGTAC 120943
Qy 531 CTGCGCATTTGTCCACGCCCAACAGTCAAGAGCCCAAGGAAACTGTGGCTGAAAGGCA 590
Db 120944 CTGCGCATTTGTCCACGCCCGCTCATCTACCGCCACCGCGCTCTCTCTCCATCCACATC 121003
Qy 591 GTCTATGTGGCGCTGTGATCCAGCGCTCTCTCTGACATATACCTGACATTCATCTTTGCC 650
Db 121004 ACCTGTGGGACCACTCTGGCTGGTGGGCTTCTCTCTGCGCTTGCAGAGATTTCTTTGCC 121063
Qy 651 GAGCTCAGCCAGGAGGAGCATCTAGTCAGGGGATGACAGGTACATCTGTGACCGCTTTAC 710
Db 121064 AAGTCAGCCAGGAGGATCAACAACTCTGCTGCCAGTTTGCACCTTCTCCCAAGAGNAC 121123
Qy 711 C---CCGATAGCCTGTGGATGGTGGTTTTCATTTCCAGCATATATAGTGGGTCTCATC 767
Db 121124 CAAGCAGAAACGATCGCTGGTTTCACTCCCGATTCTCTTACCATGTGGGGGATTCCTG 121183
Qy 768 CTGCGCGCATCTGTATCTCTCTCTGTACTGTGATCATCATCTCTAAGCTGTGCACACTCC 827
Db 121184 CTGCGCATCTGTGTGTGGCTGTGTCTAGTGGGGTAGTGACAGGTTTGCAGGCGCC 121243
Qy 828 AA---GGGCCACAGAGCGAGGCGCTCAAGACGACAGTCACTCTCATCTAGCTTTTC 884
Db 121244 CAGCGGCGCTCTCAGCGGAGAGGAGGAGTCAAGGTTGGCCATCTCTGGTGCAAGCATCTTC 121303
Qy 885 TTTGCTGTGCTGCTGCATATATATGTGGGGATCAGCATCGACTCTCTTTCATCTTTTGGGA 944
Db 121304 TTCCTCTGTGGTTCACCTTACCATCTGTCTCTCTGACACCTCTGGGAGGCTGAAG 121363
Qy 945 GTCATCAAGCAAGGATGTGATCTTCGAGAGCATTTGTGCAAGTGGATCTTCCATCAGAG 1004
Db 121364 GCGTGGACAATACCTGCAAGTGAATGTCTCTCCCGTGGCCATCACCATGTGTGAG 121423
Qy 1005 GCGCTGCGCTTCTTCCACTGTTGGCTGAAACCCCATCTCTATGCTTCTCTGGGGCAAG 1064
Db 121424 TTCTTGGGCTGGCCCACTGCTGCGCTCAACCCCATCTCTACACTTTTGGCGGCGTGAAG 121483
Qy 1065 TTCAAAAG 1072
Db 121484 TTCCGAG 121491

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RESULT 11
US-11-136-527-153
; Sequence 153, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:

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; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 153
; LENGTH: 1680
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-153

Query Match 9.4%; Score 176.4; DB 7; Length 1680;
Best Local Similarity 50.2%; Pred. No. 6.3e-25;
Matches 457; Conservative 5; Mismatches 436; Indels 12; Gaps 1;

QY 161 CTCTGAAGAGTGGGTCTGGAGACTATGACTCCACAGGAACCCCTGCTTCGGGATGA 220
DB 226 CTACGATTATGGGAAAMPAAARMWMTCTGACTCCCCGCCCTGCCACAGGACTT 285
QY 221 AAACGTCCATTTCAAATAGGATCTTCTCCGCCACCATCTACTTTCATCATCTTCTTGACTGG 280
DB 286 CAGCCTGNACTTTGACAGAACCCTTCCTGCCAGTCTCTACAGCTCTCTTTTGTGGG 345
QY 281 CATPAGTCGGAATGGATTTGGTGATCTCTGGTTCATGGGTTACCAGAAGAGCTAAGAGCAT 340
DB 346 GCTGTAGGCAATGGGCACTGGCTGTGTGCTACTGAGCGCAGCACTGCCCTGAGCAG 405
QY 341 GACGGAAGTACCGGTGACCTGTGCTGAGTGGTGTGCTCTCTTGTTCATCATCTCCC 400
DB 406 CACAGACACCTTCTGCTGCCACCTGTGGTGTGGCGATGTACTGCTGGTACTAACCTCCC 465
QY 401 CTTCTGGGCGATTGATGCCATGCTGACTGCTACTTTGGGAAATTTTGTGAAGGCTGT 460
DB 466 ACTGTGGGCAAGTAGTGTCTGCTGCCAGTGGTTTTCGGCTCTGGTCTCTGCAAGTGGC 525
QY 461 CCATATCATCTACATGTCAACCTCTACAGAGCGTTTCTCATCTGGCCTTCATCAGCCT 520
DB 526 AGGTGCCCTGTTCAACATCACTTCTACGAGGGGCTTCTGCTGGCCTGTATAAGCTT 585
QY 521 GGACCGTACTCCGATTTGTCAGGCCCAACAGCTCAAGGCCCAAGGAACTGTGGC 580
DB 586 TGACCGCTACTGAGCATAGTGCATGCCACCCAGATCTACCGCAGGAGCCCTGGGTACG 645
QY 581 TGAAGGCGAGTCTATGTGGGCGTCTGGATCCAGGCCCTCTCTGCTGACTATACCTGACTT 640
DB 646 TGTAGCCCTCACTGCAATTTGTTGTGGGCTCTCTGTGTGCTCTTTGCCCTCCAGATT 705
QY 641 CATCTTTGCCGAGCTCAGCAGGGGGAGCATCAGTCAAGGGGGATGACAGGTACATCTGTGA 700
DB 706 CATCTTCTCTGAGCCAGCCA-----TGATCAGGCGCTCAATGCCACCCCATTTG 753
QY 701 CGGCTTTACCCGATAGCCTGTGGATGGTGGTGTTCATTTCCAGCATATATGTTGG 760
DB 754 CCAGTACAACCTTCCACAGTGGGTGGACTGTCTGCGGTGTACTGAGCTAGTGGCTGG 813
QY 761 TCTCATCTCCCGGATCGTCACTCTCTCTCTGTTACTGCATCATCATCTCTAAGCTGTC 820
DB 814 TTTCTGTAGTCCCTTCTAGTCAATGGCTACTGCTATGCCCATATCTCTGGCTGTGCTGCT 873
QY 821 ACATCCAGGGCCACAGAGCGCAAGGCCCTCAAGACAGCATCTCATCTCTTCTTAC 880
DB 874 GGTCTCCAGAGGCCAGAGGGCGCTTTCAGCTATCAGGCTAGTGGTGGTGGTGGTGGC 933
QY 881 TTTCTTGTCTGCTGGCTGCATATATGTGGGATCAGCATCGACTCTCTCATCTTTT 940
DB 934 CTTTGGCGTCTGTGGACCCCTTATCACCTGGTGGTGTAGTGGATATCTTATGAGCGT 993
QY 941 GGGAGTCAAGCAAGGATGTGACTTTCGAGCATTTGTGCAAGGTGGATCTCCATCAC 1000

DB 994 GGAGATTTTGGCCCGCAACTGTGGTCGAGAAAGCCATGTGGACGTAGCCCAAGTCACTCAC 1053
QY 1001 AGAGGCCCTCGCTTCTTCCATCTGCTGCTGAACCCCATCTCTATGCTTCTCTCGGGC 1060
DB 1054 CTCAGGATGGGCTACATGCTGCTCAATCCACTGCTCTATGCTTGTGGAGT 1113
QY 1061 CAAAGTTCAA 1070
DB 1114 GAAGTTCAA 1123

RESULT 12
US-11-136-527-2373
; Sequence 2373, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2373
; LENGTH: 1324
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2373

Query Match 9.3%; Score 175; DB 7; Length 1324;
Best Local Similarity 52.2%; Pred. No. 1.1e-24;
Matches 441; Conservative 0; Mismatches 395; Indels 9; Gaps 2;

QY 222 AAGTCCTATTTCAATAGGATCTTCTGCCACCATCTACTTCATCATCTTCTTGAAGTGGC 281
DB 255 AACCTAGATATCAACAGGTATGCTGTGGTTGATATATAGTTCTGGTGAATTTGCTGAGT 314
QY 282 ATAGTCGGAATGGATTTGGTGTATCTCTGGTTCATCTGGGTTACCAGAAGAGTAAAGGAGCATG 341
DB 315 CTCGTGGGAACTCCCTGGTGTATGCTGTGTCATCTTGTACAAATCGAAGCACCTGCTCTGT 374
QY 342 ACGGACAAGTACCGGTGACCTGTGCTGAGTGGTGTGCTGCTCTCTTGTTCATCACTCCCC 401
DB 375 ACCGAGCTTACTCTGCTGAACCTGGCCATTTGCTGATCTGTCTTGGCTGACCTTGGCT 434
QY 402 TTCTGGGCGAGTTGATGCCATGGCTGCTACTTCTTGGGAAATTTTGTGAAGGCTGTC 461
DB 435 GTCTGGGCTGCATCTAAGTAATGATGGATTTTGGCTCATTTCTGTGCAAGGTATTC 494
QY 462 CATATCATCTACATGTCAACCTCTACAGAGCGTTTCTCATCTGGCCTTTCATCAGCCTG 521
DB 495 TCGTTCTCGCAGGAGATTACCTTCTACAGCAGTGTCTGTGTGCTAGCTGTCATCAGCATG 554
QY 522 GACCGTACTCTGCCATTTGTCACGCCCAACAGCTCAAGGCCAAGGAACTGCTGGCT 581
DB 555 GACCGTACTCTGCCATCTGTCACGCCCAACAGTACACTGATCCAGAAGAGACACTTGT--- 611
QY 582 GAAAAGGCGAGTCTATGTGGGCGTCTGGATCCAGGCCCTCTCTGCTGACTATACCTGACTTC 641
DB 612 GTCNAAGTTTGTGTCATCACCATGTGGTTTCTCTCACTAGTCTGTCCCTGCCCATCTTC 671
QY 642 ATCTTTGCCGAGCTCAGCAGGGGGAGCATCAGTCAAGGGGAGTACAGGTTACATCTGTGAC 701
DB 672 ATTCTTCGCACTACTCTTAAGGCCAAACCCCTTCTACCGTAGTCTGCTATGAGATATAGGT 731
QY 702 CGCCTTACCCGATAGCTGTGATGGTGTGTTCAATTCAGCATATATAGTGGGT 761
DB 732 AATAATACATCCAA-----GTGGAGGGTGGTACTCGGCATCTCGCTCAGACCTATAGGC 785


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QY 237 AGGATCTTCTGCTCCACCACTCTATCTTCTGATGCGCATAGTCGCAATGGA 236
  |||||
Db 1099 AGAGTCTTTCTACCTGCTCTTCTACAGCTGATCTTGTGCTGGCCCTGGTGGAACTTC 1040

QY 297 TTGGTGATCTGCTGATGCGGTTTACCAAGAAAGCTAAGGAGCATGACGGCAAGATCCGG 356
  |||||
Db 1039 CTCTCTAGCGGTCTTGCTCCGGTTCGTCCGCTCGAAGACGGATGACCGAGACCTATCTG 980

QY 357 CTGCACCTGTCACTGGCTGACCTCTCTTGTGTATCATCACACTCCCTTCTGGCGAGTGTAT 416
  |||||
Db 979 CTGAACCTGGCCATCTCCAACTCTCTTGTGTGTGACATGCGCTTCTGGGGCATCTCT 920

QY 417 GCCATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAAGCTGTCCATATCATCTACACT 476
  |||||
Db 919 GTGGCATGGCAATTTGGTCTTCTGGGAGGGTCTTATGCAGGTGTGAGCACCTCTATACC 860

QY 477 GTCAACCTCTACAGCAGCGTCTCATCTCGGCTTTCATCAGCTGACCGGTACCTCGCC 536
  |||||
Db 859 GTGAACCTTCTACAGTGGCATCTTCTTCTCATCAGCTGCATGAGCTGGACAAATACCTGGAG 800

QY 537 ATTGTCCAGCCACCAACAGTCAAGGCCCAAGAAACTGCTGCTGAAAAGGCAGTCTAT 596
  |||||
Db 799 ATTGTCTGGCTCGGCCCTACCAACCGACTGAGCACCGGACCGCTGTGCTTGCA 740

QY 597 GTGGCGTCTGGATCCAGCCCTCTCTGACTATACCTGACTTCTTGTGCGGACGTC 656
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Db 739 GCCAGTGTGGGCTATGGCCCTGGCTGTCTCATCTGACATGCTCTT-----GTG 686

QY 657 AGCCAGGGGACATCATGATCAGGGGGATGACAGGTATCATCTGTGACCCGCTTTACCCCGAT 716
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Db 685 AGGACGATGAGAACTCCCGCGCGTGTGGAGTGTCTATGCAGATTTTGGGGACATGGG 626

QY 717 AGCTCTGGATGCTGGTGTTCATTTCCAGCATATAATGTGGGTCTCATCTCTGCCCGC 776
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Db 625 ACCATCTGGAAGCTCTTCTCTCCGCTTCCAGCAGAACTCTCTGGGTTTCTCTCCCGCTC 566

QY 777 ATCGTATCTCTCTCTGTTACTGCTATCATCTCTAAGCTGTCACTCAAAGGGCCAC 836
  |||||
Db 565 CTTGCCATGATCTTCTTCTACTCCCGATTTGGCTCTGTGTGTGAGTCTGAGGCCCGC 506

QY 837 CAGAAAGCGAAGCCCTCAAAGCAGCAGTATCTCATCTCATCTTCTTGTGCTGTG 896
  |||||
Db 505 GGCCAGAGGGCGGCCCTGAGGATGGCGTAGCTGTGGTGGCTCTTCTTGTGCTGTG 446

QY 897 CTGCCATATTATGCGGGATCAGCATGCTCTCTCATCTTCTTGGAGTCATCAAGCAA 956
  |||||
Db 445 TTCCCGTACAATCTCACTTGTCTCTGCACTGCTGCTGCACTGCAAGCTCTTGGGGAC 386

QY 957 GGATGTGACTTCGAGACATTTGTGCAAGTGGATCTCCATCACAGAGGCCCTCGCCTTC 1016
  |||||
Db 385 TGCAAGGTCAAGCCAGCAC---CTGGACTATGCGCTGCAGGTGACGGAGCATGCGCTTC 329

QY 1017 TTCCACTGTGCTGAAACCCCATCTCTATGCTTCTCTCGGGGCCAAGTTCAAAGCTCT 1076
  |||||
Db 328 CTGCACTGTGCTTCAACCCCGCTCTACGCTTCTTCCAGCCACCGCTTCCGCCAGTAC 269

QY 1077 GCCAGCATGCACTCACTCATCATGAGGAGG 1108
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Db 268 CTCAAGGCTTTCTCGCCACTGTGCTCAGAAG 237
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RESULT 15

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US-11-136-527-4249
; Sequence 4249, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
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; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4249
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4249
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Query Match 9.0%; Score 168.6; DB 7; Length 1400;
Best Local Similarity 51.0%; Pred. No. 1.9e-23;
Matches 433; Conservative 0; Mismatches 404; Indels 12; Gaps 1;
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QY 222 AACGTCATTTCAATAGGATCTTCTCGCCACCATCTACTTCTATCATCTTCTTGACTGGC 281
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Db 7 AGCTGAACTTTGACAGAACCCTTCTGCCAGTCTCTACAGCTCTCTTTTGTGGGG 66

QY 282 ATAGTCGGCAATGGATTTGGTGTATCTCTGGTTCATGCGGTACCAAGAAGATAAGGAGCATG 341
  |||||
Db 67 CTGCTAGGCAATGGGGCAGTGGCTGTGTGTACTGAGCCAGCGCACTGCCCTGAGCAGC 126

QY 342 ACGGACAGTACGGCTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 401
  |||||
Db 127 ACAGACACCTTCTGCTCCACCTGGCTGTGGCCGATGTACTGCTGCTGCTGCTGCTGCTGCTGCT 186

QY 402 TTCTGGGCAAGTTGATGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 461
  |||||
Db 187 CTGTGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246

QY 462 CATATCATCTACATGCTCAACCTCTACAGCAGGTTCTCATCTGGCCCTTCAATCAGCCTG 521
  |||||
Db 247 GGTGCCCTGTTCACATCAACTTCTACGCGAGGGGCTTCTGCTGGCTGTATAAGCTTT 306

QY 522 GACCGGTACTCGCCATTTGTCCAGCCCAACAGTCAAGGCCAAGGAACTGCTGGCT 581
  |||||
Db 307 GACCGGTACTCGCCATTTGTCCAGCCCAACAGTCAAGGCCAAGGAACTGCTGGCTGCTGCTGCTGCT 366

QY 582 GAAAGGCGAGTCTATGTGGGCGTCTGGATCCAGCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 641
  |||||
Db 367 GTAGCCCTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 426

QY 642 ATCTTTGCGCAGCTCAGCCAGGGGACATCAGTCAAGGGGATGACAGGTACATCTGTGAC 701
  |||||
Db 427 ATCTTCTGTGAGCCAGCCATGATCAGCGCTCAATG-----CCACCCATTCG 474

QY 702 CGCTTTACCCCGATAGCTGTGGATGGTGGTGTTCATTTCCAGCATATAATGGTGGT 761
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Db 475 CAGTACAACCTTCCCACAGGTGGTGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 534

QY 762 CTCATCTCGCCGGCATCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 821
  |||||
Db 535 TTCTGATGCCCCCTTCTAGTCACTGCGCTACTGCTATGCCCATATCTCTGGCTGTGCTGCTG 594

QY 822 CACTCCAAGGGCCACAGAAAGCGCAAGGCCCTCAAGACGACAGTCACTCTATCTCTAGCT 881
  |||||
Db 595 GTCTCCAGAGGCGCAGAGGGCTTTCAGACTATGAGGCTAGTGGTGGTGGTGGTGGTGGTGGTGG 654

QY 882 TTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 941
  |||||
Db 655 TTGCGCTGTGCTGGACCCCTTATCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 714

QY 942 GGAGTCATCAAGCAAGGATGTGACTTCGAGAGCATTTGTGCAAAAGTGGATCTCCATCACA 1001
  |||||
Db 715 GGAGTTTTGGCCGGCAACTGTGGTCAGAAAGCCATGTGGACGTGACCAAGTCAAGTCACTCACC 774

QY 1002 GAGGCCCTCGCCCTTCTTCCACTGTGGCTGAAACCCCATCTCTATGCTCTCTCGGGGCC 1061
  |||||
Db 775 TCAGGCATGGGCTACATGCACTGCTGCTCAATCCACTGCTCTATGCTCTTGTGGAGTG 834

QY 1062 AAGTTCAA 1070
  |||||
Db 835 AAGTTCAA 843
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Search completed: January 11, 2006, 00:27:37
Job time : 348 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2006, 20:54:02 ; Search time 285 Seconds
(without alignments)
2239.104 Million cell updates/sec

Title: US-09-367-052-2

Perfect score: 1867

Sequence: 1 MEFISVSIYTDNYSREVG.....KRGCHSSVSTESRSSPHSS 359

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1678.5	89.9	1059	3	US-09-647-501-1
2	1678.5	89.9	1225	3	Sequence 1, Appli
3	1678.5	89.9	1664	3	Sequence 1235, Ap
4	1678.5	89.9	1664	3	US-09-582-224A-5
5	1678.5	89.9	1679	3	Sequence 5, Appli
6	1678.5	89.9	1679	3	US-09-023-655-1213
7	1678.5	89.9	1737	2	Sequence 4, Appli
8	1678.5	89.9	1737	2	US-08-202-056-4
9	1678.5	89.9	1737	2	US-08-076-093A-3
10	1678.5	89.9	1737	2	US-08-701-265-3
11	1678.5	89.9	1737	2	US-08-284-586-3

10	1678.5	89.9	1737	2	US-08-805-478-3	Sequence 3, Appli
11	1678.5	89.9	1737	2	US-08-802-627A-3	Sequence 3, Appli
12	1678.5	89.9	1737	2	US-08-801-238-3	Sequence 3, Appli
13	1678.5	89.9	1737	2	US-08-801-228-3	Sequence 3, Appli
14	1678.5	89.9	1737	3	US-09-104-296-3	Sequence 3, Appli
15	1678.5	89.9	1737	6	PCT-US94-06380-2	Sequence 2, Appli
16	1672.5	89.6	1059	3	US-09-826-509-484	Sequence 484, App
17	1672.5	89.6	1317	2	US-08-153-848-45	Sequence 45, Appl
18	1672.5	89.6	1317	3	US-09-299-843A-45	Sequence 45, Appl
19	1672.5	89.6	1317	3	US-09-088-337B-45	Sequence 45, Appl
20	1672.5	89.6	1317	6	PCT-US93-11153-45	Sequence 19, Appl
21	584	31.3	1107	3	US-09-170-496D-19	Sequence 19, Appl
22	584	31.3	1293	3	US-09-016-434-1052	Sequence 1052, Ap
23	584	31.3	1670	3	US-08-709-838-1	Sequence 1, Appli
24	584	31.3	1670	3	US-08-829-839-1	Sequence 1, Appli
25	584	31.3	1670	3	US-09-023-655-980	Sequence 980, App
26	584	31.3	1670	3	US-09-624-594-1	Sequence 1, Appli
27	584	31.3	1670	3	US-09-607-156-1	Sequence 1, Appli
28	580	31.1	1107	3	US-09-170-496D-173	Sequence 173, App
29	570.5	30.6	1607	3	US-08-875-573-19	Sequence 19, Appl
30	570.5	30.6	1607	3	US-09-764-413-19	Sequence 19, Appl
31	570.5	30.6	1677	3	US-08-939-107-33	Sequence 33, Appl
32	570.5	30.6	1677	3	US-09-016-434-1117	Sequence 1117, Ap
33	570.5	30.6	1677	3	US-09-023-655-933	Sequence 933, App
34	570.5	30.6	1677	3	US-09-067-447B-33	Sequence 33, Appl
35	570.5	30.6	1677	3	US-09-837-446-1	Sequence 1, Appli
36	570.5	30.6	1695	3	US-09-232-878-1	Sequence 1, Appli
37	551.5	29.5	1200	6	PCT-US95-03032-1	Sequence 1, Appli
38	550.5	29.5	1106	6	PCT-US92-02977-5	Sequence 5, Appli
39	550.5	29.5	1106	6	PCT-US95-03032-4	Sequence 4, Appli
40	550.5	29.5	2085	3	US-09-299-843A-65	Sequence 65, Appl
41	550.5	29.5	2085	3	US-09-088-337B-65	Sequence 65, Appl
42	546	29.2	440	3	US-09-513-999C-1915	Sequence 1915, Ap
43	544.5	29.2	1373	6	PCT-US92-02977-6	Sequence 6, Appli
44	544.5	29.2	1373	6	PCT-US95-03032-3	Sequence 3, Appli
45	544.5	29.2	1510	2	US-07-759-568-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-647-501-1
; Sequence 1, Application US/09647501

- ; Patent No. 6863887
- ; GENERAL INFORMATION:
- ; APPLICANT: No. 6863887thwest Biotherapeutics, Inc.
- ; APPLICANT: Murphy, Gerald P.
- ; APPLICANT: Boynton, Alton L.
- ; APPLICANT: Sehgal, Anil
- ; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED ON THE
- ; FILE REFERENCE: 20093-000600PC
- ; CURRENT APPLICATION NUMBER: US/09/647,501
- ; CURRENT FILING DATE: 2000-09-24
- ; PRIOR APPLICATION NUMBER: 60/079,916
- ; PRIOR FILING DATE: 1998-03-30
- ; PRIOR APPLICATION NUMBER: 60/104,656
- ; PRIOR FILING DATE: 1998-10-16
- ; NUMBER OF SEQ ID NOS: 28
- ; SOFTWARE: Patentin Ver. 2.1
- ; SEQ ID NO 1
- ; LENGTH: 1059
- ; TYPE: DNA
- ; ORGANISM: Homo sapiens
- US-09-647-501-1

Alignment Scores:
Pred. No.: 4,56e-189 Length: 1059
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 3 Gaps: 1


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Db 275 GACCTCTCTTGTGTCATCAGCTTCCCTTCTGCGAGTTGATCGCGGCAACTGGTAC 334
Qy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSer 125
Db 335 TTTGGGAACCTTCTATGCAAGGAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT 394
Qy 126 ValLeuLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 395 GTCTCTATCTGCGCTTCATCAGCTGCGACCTGCTGCGCATCGTCCAGCCACCAAC 454
Qy 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
Db 455 AGTCAGAGGCCAAGGAAGCTGTGGCTGAAAGGTGTCTATGTTGGCGTCTGATCCCT 514
Qy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 515 GCCCTCTGTCGACTATTCCTGAGCTTCATCTTGGCCAAAGCTC-----AGT 559
Qy 186 GlnGlyAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
Db 560 GAGCGAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTGTGGGTGTGTG 619
Qy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 620 TTCCAGTTTCAGACATCATGTTGGCTTATCTGCTGATGTTATGTCATCTGCTGCTG 679
Qy 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 680 TATTGATATTATCATCTCCAAAGTGTCCACTCCAGGGCCACCAGAGCGCAAGGCCCTC 739
Qy 246 LysThrThrValIleLeuIleAlaPheAlaCysTrpLeuProTyrTyrValGly 265
Db 740 AAGACACAGTATCATCTCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 799
Qy 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 800 ATCAGATCGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 859
Qy 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysLysLeuAsn 305
Db 860 ACTGTGCACAAAGTGGATTTCCATCAGCGAGCCCTAGCTTCTTCCACTGTTGCTGAAC 919
Qy 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 920 CCATCTCTATGCTTTCTTGGAGCCAAATTTAAACCTCTGCCCCAGCAGCAGCTCACC 979
Qy 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
Db 980 TCTGTGAGCAGAGGCTCCAGCTCAGATCTCTCCAAAGGAAGCGAGGTGAGCATTTCA 1039
Qy 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1040 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCCTCCAGC 1081
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RESULT 3

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US-09-582-224A-5
; Sequence 5, Application US/09582224A
; Patent No. 6429308
; GENERAL INFORMATION:
; APPLICANT: IJIMA, Osamu
; APPLICANT: GOTO, Takeshi
; APPLICANT: SHIMADA, Takashi
; TITLE OF INVENTION: HIV Infection Inhibitors
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/582,224A
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: PCT/JP99/06534
; PRIOR FILING DATE: 1999/11/24
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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1664
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA of CXCR4
US-09-582-224A-5

Alignment Scores:
Pred. No.: 9,01e-189 Length: 1664
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 3 Gaps: 1
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US-09-367-052-2 (1-359) x US-09-582-224A-5 (1-1664)

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Qy 6 ValSerIleTyrThrSerAspAenTyrSerGluValGlySerGlyAspTyrAspSer 25
Db 86 ATCAGTATATACACTTCAGATACTACCGAGGAAATGGCTCAGGGACTATGACTCC 145
Qy 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 146 ATGAAGGAACCCCTGTTTCCGTGAAGAAATGCTAATTTCAATAAAATCTTCTGCCACC 205
Qy 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 206 ATCTACTCCTCATCTTCTTAATCTGCAATTTGGGCAATGGATTGTTGTTCTCTGTCATG 265
Qy 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 266 GGTACCAGAGAAACTGAGAGCATGACGGAACAGTACAGGCTGCACCTGTGAGTGCC 325
Qy 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
Db 326 GACCTCTCTTGTGTCATCAGCTTCCCTTCTGCGCAGTTGATGCGCGTGAACCTGGTAC 385
Qy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 386 TTTGGGAACCTTCTATGCAAGGAGTCCATGTCATCTACAGTCAACCTCTACAGCAGT 445
Qy 126 ValLeuLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 446 GTCTCTATCTGCGCTTTCATCAGTCTGACCGCTACCTGCGCCATCGTCAGCGCCACCAAC 505
Qy 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
Db 506 AGTCAGAGGCCAAGGAAGCTGTGGCTGAAAGGTGTCTATGTTGGCGTCTGAGTCCCT 565
Qy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 566 GCCCTCTCTGACTATTCCTGACTTCTTTCCTGCAAGCTC-----AGT 610
Qy 186 GlnGlyAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
Db 611 GAGCGAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTGTGGGTGTGTG 670
Qy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 671 TTCCAGTTTCAGACATCATGTTGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 730
Qy 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 731 TATTGATATTATCATCTCCAAAGTGTCCAAAGCTCCAGGGCCACCAGAGCGCAAGGCCCTC 790
Qy 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
Db 791 AAGACACAGTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850
Qy 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
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Db 851 ATCAGCATCGACTCTCTTCATCTCTCTGGAATCATCAAGCAAGGGTGTGAGTTGAGAAC 910
QY 286 lIeValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 911 ACTGTGCACAAGTGGATTTCCATCACCAGGAGCCCTAGCTTTCTTCCACTGTGTGCTGAAC 970
QY 306 ProIleLeuTyAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 971 CCATCTCTATGCTTCTCTTGAGGCAAAATTTAAACCTCTGCCAGCAGCAGCTCACC 1030
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
Db 1031 TCTGTGAGCAGAGGCTCCAGCTCCAGATCTCTCCAAAGGAAGCGAGGTGGACATTCA 1090
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1091 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1132
RESULT 4
US-09-023-655-1213
; Sequence 1213, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1213:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1664 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9219868
US-09-023-655-1213
Alignment Scores:
Pred. No.: 9,01e-189 Length: 1664
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11

Query Match: 89.90% Indels: 5
DB: 3 Gaps: 1
US-09-367-052-2 (1-359) x US-09-023-655-1213 (1-1664)
QY 6 ValSerIleTyThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
Db 86 ATCAGTATATACATTCAGATAACTACACCGAGGAAATGGGCTCAGGGGACTATGACTCC 145
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 146 ATGAAGGACACCTGTTCGTAAGAAATGTAATTTCAATAAAATCTTCCTGCCACC 205
QY 46 lIeTyThrPheIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 206 ATCTACTCCATCATCTTTAACTGGCATTTGGGCATGGATTTGGTCTATCTGGTCTATG 265
QY 66 GlyTyThrGlnLysLeuArgSerMetThrAspLysTyThrArgLeuHisLeuSerValAla 85
Db 266 GGTATTACCAAGAAACTGAGAAGCATGACGGAAGTACAGGCTGCACCTGTCACTGGGCC 325
QY 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
Db 326 GACCTCCTCTTTGTTCATCACGCTTCCTTCTGGGAGTTGATGCCGTGGCAACTGGTAC 395
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyThrValAsnLeuTyThrSer 125
Db 386 TTGGGAACCTTCTATGAAAGCAGTCCATGTCATCTACACAGTCAACTCTACAGCAGT 445
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyThrLeuAlaIleValHisAlaThrAsn 145
Db 446 GTCTCATCTGGCCTTTCATGATGTCGACCGCTACCTGGCCATCTGCACGCCACCAAC 505
QY 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyThrValGlyValTrpIlePro 165
Db 506 AGTCAGAGGCCAAGGAAGCTGTGGCTGAAAGGTGGTCTATGTTGGCTGTGGATCCCT 565
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 566 GCCCTCCTGCTGACTATTCCGACTTCATCTTTGCCAAGCTC-----AGT 610
QY 186 GlnGlyAspAspArgTyThrIleCysAspArgLeuTyThrProAspSerLeuTrpMetValVal 205
Db 611 GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTGTGGGTGTGTG 670
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 671 TTCCAGTTTCAGCACATCATGTTGGCTTATCTCTGCCCTGGTATTGTCTATCTCTCTGC 730
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 731 TATTGCAATTATCATCTCCAGCTGTACACTCCAGGGCCACCAGAGCGCAAGGCCCTC 790
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyThrValGly 265
Db 791 AAGACCACAGTCATCTCTCTGCTTCTTCGCTGTGTGGCTGTGTGCTTACTACATTGGG 850
QY 266 lIeSerIleAspSerPheIleLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 851 ATCAGCATCGACTCTTCATCTCTCTGGAATCATCAAGCAAGGGTGTGAGTTTGAAC 910
QY 286 lIeValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 911 ACTGTGCACAAGTGGATTTCCATCACCAGGAGCCCTAGCTTTCTTCCACTGTGTGCTGAAC 970
QY 306 ProIleLeuTyAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 971 CCATCTCTATGCTTCTCTTGAGGCAAAATTTAAACCTCTGCCAGCAGCAGCTCACC 1030
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
Db 1031 TCTGTGAGCAGAGGCTCCAGCTCTCAAGATCTCTCCAAAGGAAGCGAGGTGGACATTCA 1090

QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
DB 1091 TCTGTTTCCAGTCTGAGTCTTCAAGTTTTCCTCCAGC 1132

RESULT 5

US-09-517-605-14
; Sequence 14, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Tneo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-517-605-14

Alignment Scores:

Pred. No.: 9,13e-189 Length: 1679
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 3 Gaps: 1

US-09-367-052-2 (1-359) x US-09-517-605-14 (1-1679)

QY 6 ValSerIleThrSerAspIleThrGluValGlySerGlyAspThrAspSer 25
DB 98 ATCAGTATATACACTTTCAGATACACCGAGGAAATGGCTCAGGGGACTATGACTCC 157
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 158 ATGAGGAACCCCTGTTCCGTGAAGAAATGCTATTTCAATAAAATCTCTGCCACC 217
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
DB 218 ATCTACTCCATCATCTTTAACTGCAATGTGGCAATGGATTGCTCATCTGGTCTAG 277
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysThrArgLeuHisLeuSerValAla 85
DB 278 GGTACCAAGAAACTGAGAGCATGACGGACAGTACAGGCTGCACCTGTCTAGTGGCC 337
QY 86 AspLeuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTrpTyr 105
DB 338 GACCTCTCTTGTGATCATCGCTTCCCTTCTGGGCAATGATGCCGTGCAACTGGTAC 397
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
DB 398 TTGGGAACCTTCTATGCAAGGAGTCCATGTCATCATCACAGTCAACTCTACAGCACT 457
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
DB 458 GTCTCATCTGGCCCTTCTATCATCTGACCGCTACCTGCGCCATCTGCCACGCAAC 517
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
DB 518 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAGGTGCTATGTTGGCGTCTGGATCCCT 577
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
DB 578 GCCCTCTGCTGACTATTCGAGCTTCATCTTTGCCAAGCTC-----AGT 622
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205

DB 623 GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGTGTG 682
QY PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
DB 683 TTCCAGTTTCCAGCAGCATCATGTTGGCTTATCTCTGCTGGTATTGCTCATCTGCTGTC 742
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 743 TATTGCAATTATCATCTCCAAGCTGTCACTCCAGGGCCACCAAGAGCGCAAGGCCCTC 802
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
DB 803 AGACCACAGTATCTCTCATCTCTGCTGCTTCTGCTGCTGCTGCTTACTACATTGGG 862
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
DB 863 ATCAGCATCGACTCTCTCATCTCTGGAATCATCAAGCAGGGTGTGAGTTTGAGAAC 922
QY 286 IleValHisIleTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 923 ACTGTGCACAAGTGGATTTCATCATCCAGGAGCCCTAGCTTTCTTCCACTGTTGCTGTAAC 982
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
DB 983 CCCATCTCTATGCTTCTCTGGAGCCAAATTTAAACCTCTGCCAGCACGCACTCAC 1042
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
DB 1043 TCTGTGAGCAGAGGGTCCAGCTCAGATCTCTCCAAAGGAAGCGAGGTGACATTC 1102
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
DB 1103 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCCTCCAGC 1144

RESULT 6
US-08-202-056-4
; Sequence 4, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168


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US-09-367-052-2 (1-359) x US-08-076-093A-3 (1-1737)
QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
DB 100 ATCAGTATATACACTTCAGATAACTACACCGAGAAATGGCTCAGGGGACTATGACTCC 159
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 160 ATGAAGGAACCTGTTTCGCGTGAAGAAATGCTAAATTTCAATAAAATCTTCCTGCCACC 219
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
DB 220 ATCTACTCCATCATCTTCTTAACCTGGCATTTGGGCAATGATTTGGTCATCTCGTCATG 279
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
DB 280 GGTATACCAGAAGAACTGAGAGCATCGACGACAAGTACAGGCTGCACCTGTCACTGCC 339
QY 86 AspLeuLeuPheValIleThrLeuProPheTyrPheValAlaAspAlaMetAlaAspTyr 105
DB 340 GACCTCTCTTGTGTCATCGCTTCCCTTCTGGGCACTTGTATGCGTGGCAAACTGTGATC 399
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
DB 400 TTTGGGAACTTCTATCAAGGCAAGTCCATGTCTATCTACAGCTCAACCTCTCAGCAGT 459
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
DB 460 GTCTCTATCTGGCTTCATCAGCTGACCGCTACTCTGGCCATCGTCCAGGCCAAC 519
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrPhePro 165
DB 520 AGTCAGAGGCCAAGGAGCTGTGGCTGAAAGGTGCTCTATGTGGCGTCTGATCCCT 579
QY 166 AlaLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 195
DB 580 GCCCTCTCTGTGACTATVTCGCACTTCATCTTGGCAACGTC-----AGT 624
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValVal 205
DB 625 GAGGCAGATCAGACATATATCTGTGACCGCTTCTACCCCAATGACTGTGGGTGTGTG 684
QY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225
DB 685 TTCCAGTTTCAGCACATCATGGTTGGCTTATCTGCTGGTATGTGTCATCTCTCTGCTGC 744
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 745 TATTGCATTATCATCTCCAAGCTGTACACTCCAAGGGCCACCAGAAAGCGCAAGGCCCTC 804
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrLeuProTyrTyrValGly 265
DB 805 AAGACACAGATCATCTCTCTGGCTTCTTCTGCTGTGGTGGCTTACTACTATGTTGG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
DB 865 ATCAGCATCGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 924
QY 286 IleValHisLysTyrPheIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 925 ACTGTGCACAAGTGGATTTCCATCACCAGGCGCTAGCTTTCTTCCACTCTGTGTCTGAAC 984
QY 306 ProfileLeuTyrAlaPheLeuGlyAlaLysPheLysSerAlaGlnHisAlaLeuAsn 325
DB 985 CCATCTCTATGCTTCTTCTGGGCAAAATTTAAACCTCTGCCCAGCAGCACTCACC 1044
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
DB 1045 TCTGTGAGCAGAGGTCACGCTCAAGATCTCTCCAAAGGAAGCGAGGTGACATTCA 1104
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
DB 1105 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1146

RESULT 8
US-08-701-265-3
; Sequence 3, Application US/08701265
; Patent No. 5776457
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PP4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,265
; FILING DATE: 22-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 nucleotides
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-701-265-3

Alignment Scores:
Pred. No.: 9,61e-189 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 2 Gaps: 1

US-09-367-052-2 (1-359) x US-08-701-265-3 (1-1737)
QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
DB 100 ATCAGTATATACACTTCAGATAACTACACCGAGAAATGGCTCAGGGGACTATGACTCC 159
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 160 ATGAAGGAACCTGTTTCGCGTGAAGAAATGCTAAATTTCAATAAAATCTTCCTGCCACC 219
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
DB 220 ATCTACTCCATCATCTTCTTAACCTGGCATTTGGGCAATGATTTGGTCATCTCGTCATG 279
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
DB 280 GGTATACCAGAAGAACTGAGAGCATCGACGACAAGTACAGGCTGCACCTGTCACTGCC 339
QY 86 AspLeuLeuPheValIleThrLeuProPheTyrPheValAlaAspAlaMetAlaAspTyr 105
DB 340 GACCTCTCTTGTGTCATCGCTTCCCTTCTGGGCACTTGTATGCGTGGCAAACTGTGATC 399
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
DB 400 TTTGGGAACTTCTATCAAGGCAAGTCCATGTCTATCTACAGCTCAACCTCTCAGCAGT 459
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
DB 460 GTCTCTATCTGGCTTCATCAGCTGACCGCTACTCTGGCCATCGTCCAGGCCAAC 519
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrPhePro 165
DB 520 AGTCAGAGGCCAAGGAGCTGTGGCTGAAAGGTGCTCTATGTGGCGTCTGATCCCT 579
QY 166 AlaLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 195
DB 580 GCCCTCTCTGTGACTATVTCGCACTTCATCTTGGCAACGTC-----AGT 624
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValVal 205
DB 625 GAGGCAGATCAGACATATATCTGTGACCGCTTCTACCCCAATGACTGTGGGTGTGTG 684
QY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225
DB 685 TTCCAGTTTCAGCACATCATGGTTGGCTTATCTGCTGGTATGTGTCATCTCTCTGCTGC 744
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 745 TATTGCATTATCATCTCCAAGCTGTACACTCCAAGGGCCACCAGAAAGCGCAAGGCCCTC 804
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrLeuProTyrTyrValGly 265
DB 805 AAGACACAGATCATCTCTCTGGCTTCTTCTGCTGTGGTGGCTTACTACTATGTTGG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
DB 865 ATCAGCATCGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 924
QY 286 IleValHisLysTyrPheIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 925 ACTGTGCACAAGTGGATTTCCATCACCAGGCGCTAGCTTTCTTCCACTCTGTGTCTGAAC 984
QY 306 ProfileLeuTyrAlaPheLeuGlyAlaLysPheLysSerAlaGlnHisAlaLeuAsn 325
DB 985 CCATCTCTATGCTTCTTCTGGGCAAAATTTAAACCTCTGCCCAGCAGCACTCACC 1044
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
DB 1045 TCTGTGAGCAGAGGTCACGCTCAAGATCTCTCCAAAGGAAGCGAGGTGACATTCA 1104
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
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Db 220 ATCTACTCCATCATCTTCTTAACCTGCGCATTTGTGGCAATGGATTGGTCATCTCTGGTCATG 279
Qy 66 GlyTyrGlnIlyslsLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 280 GGTACCAAGAAACTGAGAGCACTGACGAGCAAGTACAGGCTGCACCTGTCAAGTGGCC 339
Qy 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
Db 340 GACCTCTCTTGTGTATCATCGCTTCTCTCTGCGCAGTTGATCGCTGCGCAACTGGTAC 399
Qy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSer 125
Db 400 TTTGGGAACCTTCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT 459
Qy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 460 GTCTCTCATCTGCGCTTCTATCATGCTGAGCCGCTACTCTGCGCCATCTGCACGCCACCAAC 519
Qy 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrrpIlePro 165
Db 520 AGTCAGAGCCCAAGAAAGCTGTGTGGCTGAAGAGTGTCTATGTTGGCTGTGGATCCCT 579
Qy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 580 GCGCTCTGCTGACTATTCGCGACTTCTCATCTTTGCCAACGTC-----AGT 624
Qy 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
Db 625 GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTGTGGGTGTGTG 684
Qy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 685 TTCCAGTTTCAGCACATCATGTTGGCTTATCTGCTGGTATTGTCTCTCTGCTGCTGC 744
Qy 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 745 TATTGCATTATCATCTCCAAGCTGTCCACTCCCAAGGGCCACCAGAAGCGCAAGGCCCTC 804
Qy 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
Db 805 AAGACCACAGTATCTCATCTCTGCTGCTTCTGCTGCTGCTGCTTACTACTATGGG 864
Qy 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 865 ATCAGCATCGACTCTCTCTATCTCTCTGGAATCATCAAGCAAGGGTGTGATTTGAGAAC 924
Qy 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 925 ACTGTGCACAAAGTGGATTTCCATCACCGAGGCCCTAGCTTCTTCCACTGTTGCTCTGAAC 984
Qy 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 985 CCATCTCTATGCTTCTCTTGGAGCCAAATTTTAAACCTCTCTCCCAAGCAGCACTCAC 1044
Qy 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
Db 1045 TCTGTGAGCAGAGGGTCCAGCTCAAGATCTCTCCAAAGAAAGGAGGTGGACATTCA 1104
Qy 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1105 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTCTTCACTCCAGC 1146

RESULT 9

US-08-284-586-3

; Sequence 3, Application US/08284586

; Patent No. 5840856

; GENERAL INFORMATION:

; APPLICANT: Chuntharapai, Anan

; APPLICANT: Lee, James

; APPLICANT: Hebert, Caroline

; APPLICANT: Jin Kim, K.

; TITLE OF INVENTION: Antibodies to Human PF4A Receptors

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,586
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 nucleotides
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-284-586-3

Alignment Scores:

Pred. No.: 9,61e-189 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 2 Gaps: 1

US-09-367-052-2 (1-359) x US-08-284-586-3 (1-1737)

Qy 6 ValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGlyAspTyrAspSer 25
Db 100 ATCAGTATATACATTCAGATACACCGAGGAATGGCTCAGGGAGACTATGACTCC 159
Qy 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 160 ATCAAGAACCCCTGTTCCGTGAGAAATGCTAATTTCAATAAAATCTTCTCGCCACC 219
Qy 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 220 ATCTACTCCATCATCTTCTTAATCTGCAATTTGGCAATGGATTTGCTATCTCTGGTCATG 279
Qy 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 280 GGTACCAAGAAACTGAGAGCACTGAGAGCATGACGAGCAAGTACAGGCTGCACCTGTCAAGTGGCC 339
Qy 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
Db 340 GACCTCTCTTGTGTATCATCGCTTCTCTCTGCGCAGTTGATCGCTGCGCAACTGGTAC 399
Qy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 400 TTTGGGAACCTTCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT 459

QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrIleuAlaIleValHisAlaThrAsn 145
DB 460 GTCTCTATCTGGCTTTTCATCAGCTGACCGCTACCTGGCCATCGTCCACGCCCAAC 519
QY 146 SerGlnArgProArgLysLeuAlaGluLysAlaValTyrValGlyValTrrPlePro 165
DB 520 AGTCAGAGGCCAAGAAAGCTGTGGCTGAAAGGTGTCTATGTGGCGTCTGGATCCCT 579
QY 166 AlaLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
DB 580 GCCTCTCTGCTGACTATTCGCGACTTCATCTTTGCCAACGTC-----AGT 624
QY 186 GlnGlyAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrrPleMetValVal 205
DB 625 GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGGTGTG 684
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
DB 685 TTCAGTTTCAGCACATCATGGTGGCTTATCTGCTGGTATGTTCCTGCTCTGCTGC 744
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 745 TATTGCATTATCATCTCCAGCTGTACACTCCAGAGGCCACCAAGCGCCAGGCCCTC 804
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
DB 805 AAGACACAGTATCTCTCATCTGGCTTCTTCTGCGCTGTGGCTGCTTACTACATTGGG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
DB 865 ATCAGATCTGACCTCTTCATCTCTCTGGAATCATCAAGCGGCTGAGTTTGAGAAC 924
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 925 ACTGTGCACAGTGGATTTCATCATCAGCGGCCCTAGCTTCTTCCACTGTCTCTGAAC 984
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
DB 985 CCCATCTCTATGTTTCTTGTGGAGCCAAATTTAAACCTCTGCCAGCAGCACTCACC 1044
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
DB 1045 TCTGTGAGAGAGGGTCCAGCTCCAGATCCTCTCCAAAGAAAGCGAGGTGACATTCA 1104
QY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
DB 1105 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1146

RESULT 10

US-08-805-478-3
; Sequence 3, Application US/08805478
; Patent No. 5874543
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/805,478
; FILING DATE: 25-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-805-478-3

Alignment Scores:

Pred. No.: 9 61e-189 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 2 Gaps: 1

US-09-367-052-2 (1-359) x US-08-805-478-3 (1-1737)

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGlyAspTyrAspSer 25
DB 100 ATCATGATATATACATCTTCAGATACTACCGAGGAAATGGCTCAGGGACTATGACTCC 159
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 160 ATGAAGGAACCCCTGTTTCCGTGAAGAAATGCTTAATTTCAATAAAATCTTCTCGCCACC 219
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
DB 220 ATCTATCTCATCTTCTTAACTGGCATTTGGGCAATGGATGGTTCATCTCTGGTCATG 279
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
DB 280 GGTACCAGAGAAACTGAGAGCATGACGACAGTACAGGCTGCACCTGTCTAGTGGCC 339
QY 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrrPyr 105
DB 340 GACCTCTCTTTGTCTCATCGCTTCCCTTCTTGGGCAGTTGATCCCGTGGCAAACTGGTAC 399
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
DB 400 TTTGGGAACCTTCTTATGCAAGGCGATGTCATCTACACAGTCAACCTCTACAGAGT 459
QY 126 ValIleLeuLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
DB 460 GTCTCTATCTGGCCCTTCATCATCTGGACCGCTACCTGGCCATCGTCCACGCCCAAC 519
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrrPlePro 165
DB 520 AGTCAGAGGCCAAGAAAGCTGTGGCTGAAAGGTGTCTATGTGGCGTCTGGATCCCT 579
QY 166 AlaLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
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Qy 266 IleserIleAaspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAaspPheGluSer 285
Db 865 ATCAGCATCGACTCTTCTCATCTCTCGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC 924
Qy 286 IlevaHIsIysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAen 305
Db 925 ACTGTGCACAAGTGGATTTCCATCACCAGGCGCTAGCTTTCTTCCACTGTGTGCTGAAC 984
Qy 306 ProIleLeuTyAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAen 325
Db 985 CCATCTCTATGTTTCTTGGAGCCAAATTTAAACCTCTGCCAGCAGCACTCACC 1044
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Db 1045 TCTGTGAGCAGAGGTCAGGCTCAGATCTCTCCAAAGGAAAGCGAGGTGCACATTC 1104
Qy 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
Db 1105 TCTGTTTCCACTGAGTGTGAGTCTTCAAGTCTTCACTCCAGC 1146

RESULT 12

US-08-801-238-3
; Sequence 3, Application US/08801238
; Patent No. 5919896
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPacIn (Genentech)
; APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1D1
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELETYPE: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-801-238-3

Alignment Scores: 9.61e-189 Length: 1737
Pred. No.: 1678.50 Matches: 319
Score: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 2 Gaps: 1
US-09-367-052-2 (1-359) x US-08-801-238-3 (1-1737)
Qy 6 ValSerIleTyThrSerAaspSerGluGluValGlySerGlyAaspTyAaspSer 25
Db 100 ATCAGTATATACACTTCAGATACTACACCGAGGAAATGGGCTCAGGGGACTATGACTCC 159
Qy 26 AsnLysGluProCysPheArgAaspGluAenValHisPheAenArgIlePheLeuProThr 45
Db 160 ATGAAGGAACCCCTGTTTCCGTGAAGAAATGCTAAATTTCAATAAATCTTCTCTGCCACC 219
Qy 46 IleTyPheIleIlePheLeuThrGlyIleValGlyAenGlyLeuValIleLeuValMet 65
Db 220 ATCTACTCCATCATCTTCTTAACCTGGCATTTGGGCAATGGATTGGTCATCTCTGGTCATG 279
Qy 66 GlyTyGlnLysLysLeuArgSerMetThrAaspLysTyArgLeuHisLeuSerValAla 85
Db 280 GGTATACAGAAAGAACTGAGACATGACGACAGTACAGGCTGCACCTCTCAGTGGCC 339
Qy 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAaspAlaMetAlaAaspTrpTy 105
Db 340 GACCTCTCTTTGTGTCATCAGCTTCCCTTCTGGGCAAGTTGATGCCCTGGCAAACTGGTAC 399
Qy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyThrValAenLeuTySerSer 135
Db 400 TTTGGGAACCTTCTATGCAAGGAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT 459
Qy 126 ValLeuLeuAlaPheIleSerLeuAaspTyArgTyLeuAlaIleValHisAlaThrAen 145
Db 460 GTCTCTCTGCGCTTCATCATCTGAGCCGCTACCTGCGCATCTCCAGCCACCAAC 519
Qy 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyValGlyValTrpIlePro 165
Db 520 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAGGTGCTCTATGTTGGCTCTGGATCCCT 579
Qy 166 AlaLeuLeuLeuThrIleProAaspPheIlePheAaspValSerGlnGlyAaspIleSer 185
Db 580 GCCTCTCTGCTGACTATTCCGACTTTCATCTTTGCCAAGCTC-----AGT 624
Qy 186 GlnGlyAaspArgTyIleCysAaspArgLeuTyProAaspSerLeuTrpMetValVal 205
Db 625 GAGGCAGATGACAGATATATCTGTGACCCCTTCTACCCCAATGACTTGGGGTGGTTGTG 684
Qy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 685 TTCCAGTTTTCAGCACATCATCTGTTGGCTTATCTCTGCTGGTATTGTCATCTCTGCTGTC 744
Qy 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 745 TATTGCAATTATCATCTCCAAGCTGTCCACACTCCAAGGGCCACCAGAAAGCGCAAGGCCCTC 804
Qy 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyTyTyValGly 265
Db 805 AGACACACAGTATCTCTGCTGCTTCTTCTGCTGCTTCTGCTGCTTCTTCTACTACTATGGG 864
Qy 266 IleSerIleAaspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAaspPheGluSer 285
Db 865 ATCAGCATCGACTCTCTTCATCTCTCTGGAATCATCAAGCAAGGGTGTGAGTTTGAGAAC 924
Qy 286 IlevaHIsIysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAen 305
Db 925 ACTGTGCACAAGTGGATTTCCATCACCAGGCGCTAGCTTTCTTCCACTGTGTGCTGAAC 984
Qy 306 ProIleLeuTyAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAen 325
Db 985 CCATCTCTATGCTTTCTTGGAGCCAAATTTAAACCTCTTGGCCAGCAGCACTCACC 1044

QY 326 SerMetSerArgGlySerSerLeuValLeuLeuSerLysGlyLysArgGlyGlyHisSer 345
Db 1045 TCTGTGAGCAGAGGGTCCAGCCTCAGATCCTCTCCAAAGGAAGCGAGGTGACATTCA 1104
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1105 TCTGTTTCCACTGAGTCTTCAAGTTTTCACCTCCAGC 1146

RESULT 13
US-08-801-228-3
; Sequence 3, Application US/08801228
; Patent No. 5922541
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
; TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,228
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELETYPE: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-801-228-3

Alignment Scores:
Pred. No.: 9,61e-189 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservatives: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 2 Gaps: 1

US-09-367-052-2 (1-359) x US-08-801-228-3 (1-1737)

QY 6 ValSerIleThrSerAspAsnTyrSerGluValGlySerGlyAspTyrAspSer 25
Db 100 ATCAGTATATACACTTTCAGATACTACACCGGAAATGGGCTCAGGGGACTATGACTCC 159

QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 160 ATGAGGAACCTGTTTCGTGAGGAATAATGTAATTTCAATAAATCTTCTGCCCCACC 219
QY 46 IleTyrPheIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 220 ATCTACTCCATCATCTTCTTAACGTGGCAATGGATGGTTCATCTCTGTCATG 279
QY 66 GlyTyrGlnLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 280 GGTACCAGAGAAACTGAGAACATGACGACAGTACAGGCTGCACCTGTCTCAGTGGCC 339
QY 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
Db 340 GACCTCTCTTTGTCTATCAGCTTCCCTCTGGCAGTTGATGCGGTGGCAAACTGGTAC 399
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 400 TTTGGGAACCTTCTATGCAAGCAGTCCATGTCTACACAGTCAACCTCTACAGCAGT 459
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 460 GTCTCTCATCTGCGCTTCTATGTCAGTCTGGACCGCTACCTGGCCATCGTCCAGCCACAAC 519
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
Db 520 AGTCAGAGCCCAAGNAGCTGTGGCTGAAAGGTGGTCTATGTTGGCGCTGCGATCCCT 579
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 195
Db 580 GCGCTCTCTGCTGACTATTCCTGACTCTATCTTTGCCAAGTCTCTCTCTCTCTCTCTCT 624
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
Db 625 GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTGTGGGGTGTG 694
QY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225
Db 685 TTCCAGTTTCAGCACATCATGTTGGCTTATCTGCTGTTGTTGTTGTTGTTGTTGTTG 744
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 745 TATTGCATTATCATCTCCAAGCTGTCCACTCCAGGGCCACCCAGAGGCGCAAGGCCCTC 804
QY 246 LysThrThrValIleLeuIleLeuAlaPheAlaCysTrpLeuProTyrTyrValGly 265
Db 805 AAGACCACAGTCTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 865 ATCAGCATCGACT 924
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 925 ACTGTGCACAAAGTGGATTTCCATCACCGAGGCCCTAGCTTCTCTCCACTGTTGTTG 984
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 985 CCCATCTCTATGCTTCTCTGAGCCAAATTTAAACCTCTGCCCCAGCAGCAGCTCACC 1044
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
Db 1045 TCTGTGAGCAGAGGGTCCAGCCTCAGATCCTCTCCAAAGGAAGCGAGGTGACATTCA 1104
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1105 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1146

RESULT 14

US-09-104-296-3
; Sequence 3, Application US/09104296
; Patent No. 6087475

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Qy 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
Db 340 GACCTCTCTTTGTTCATCAGCTTCCCTTCTGGCAGTTGATGCGGTGGCAAACTGGTAC 399
Qy 106 PheGlyIysPheLeuCysIysAlaValHisIleIleTyrThrValAanLeuTyrSerSer 125
Db 400 TTTGGGAACCTTCTATGTCAGAGGAGTCCATGTCTATCTACAGTCAACCTCTACAGCAGT 459
Qy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 460 GTCTCATCTCGCCTTCATCAGTCTGGACCGCTACTCTGGCCATCTGTCACGCCACCAAC 519
Qy 146 SerGlnArgProArgIysLeuLeuAlaGluIysAlaValTyrValGlyValTrpIlePro 165
Db 520 AGTCAGAGGCCAAGGAAGCTTTGGCTGAAAAGGTGGTCTATGTGGCGTCTGGATCCCT 579
Qy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 580 GCCTCTCTGTCTACTATTTCCCGACTTTCCTCATCTTTGCCAACGTC-----AGT 624
Qy 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
Db 625 GAGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTGTGGGTGGTTGTG 684
Qy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 685 TTCCAGTTTCAGCACATCATGTTGGCTTATCTCGCTGATTTGTCATCTCTGCTCTGC 744
Qy 226 TyrCysIleIleIleSerIysLeuSerHisSerIysGlyHisGlnIysArgIysAlaLeu 245
Db 745 TATTGCAATTATCATCTCCAAGCTGTCCACACTCCAAGGGCCACCAGAAGCAAGGCCCTC 804
Qy 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
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Qy 266 IleSerIleAspSerPheIleLeuLeuGlyValIleIysGlnGlyCysAspPheGluSer 285
Db 865 ATCAGCATCGACTCTTCATCTCTCTGGAATCATCAAGCAAGGGTGTGAGTTTGAGAAC 924
Qy 286 IleValHisIysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAan 305
Db 925 ACTGTGCACAAAGTGGATTTCCATCAGCGAGCCCTAGCTTTCTTCCACTGTGTCTGAAC 984
Qy 306 ProIleLeuTyrAlaPheLeuGlyAlaIysPheIysSerSerAlaGlnHisAlaLeuAan 325
Db 985 CCATCTCTCTATGCTTCTCTGTGAGCGCAATTTAAACCTCTGCCACGACGACTCACC 1044
Qy 326 SerMetSerArgGlySerSerLeuIysIleLeuSerIysGlyIysArgGlyGlyHisSer 345
Db 1045 TCTGTGACGAGAGGTTCAGCCTCAAGATCTCTCCAAAGGAAGCGAGGTGGACATTCA 1104
Qy 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1105 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCCTCCAGC 1146

RESULT 15
PCT-US94-06380-2
; Sequence 2, Application PC/TUS9406380
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: K. Jin Kim
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY DISORDERS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco

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STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM pc compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06380
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-06380-2

Alignment Scores:
Pred. No.: 9,61e-189 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 6 Gaps: 1

US-09-367-052-2 (1-359) x PCT-US94-06380-2 (1-1737)

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DB     100 ATCAGTATATACATCTTCAGTAACTACACCGAGGAAATGGGCTCAGGGGACTATGACTCC 159

QY     26 AsnLysGluProCysPheArgAspGluAsnValHiePheAsnArgIlePheLeuProThr 45
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     160 ATGAAGGAACCCCTGTTTCCGTGAAGAAATGCTAAATTTCAATAAAATCTTCTGCCACC 219

QY      46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     220 ATCTATCCATCATCTTCTTAACTGGGCAATGTTGGCAATGGATGGTTCATCTGGTCATG 279

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QY      86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
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QY     106 PheGlyLysPheLeuCysLysAlaValHieIleIleTyrThrValIleLeuTyrSerSer 125
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DB     400 TTGGGAACCTTCTATGCAAGGCAGTCCATGTCTATCTACACAGTCAACCTCTCAGCAGT 459

QY     126 ValIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
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DB     460 GTCTCTATCTGGCCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCCAAC 519

QY     146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
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Search completed: January 11, 2006, 00:32:36

Job time : 300 secs

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QY     186 GlnGlyAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     625 GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTGTGGGTGGTGTG 684

QY     206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     685 TTCCAGTTTCAGCACATCATGTGTGGCCTTATCTCGCCTGGTATGTCATCTCTGCTCTGC 744

QY     226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     745 TATTGCATTTATCATCTCCAAAGCTGTGCACACTCCNAGGGCCACCAAGCGCAAGGCCCTC 804

QY     246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY     266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     865 ATCAGCATCGACTCTTCTCTCTCTGGAATCATCAAGCAAGGGGTGAGATTGAGAAC 924

QY     286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     925 ACTGTGCACAAAGTGGATTTCCATCACCAGGAGGCCCTAGCTTTCTTCCACTGTGTCTGAAC 984

QY     306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     985 CCCATCTCTATGCTTTCCTTGGAGCCAAATTTAAACCTCTGCCCGACGACGACTCACC 1044

QY     326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
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DB     1045 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAGCGAGGTGACATTCA 1104

QY     346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB     1105 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1146
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 11, 2006, 00:22:05 ; Search time 1042 Seconds
(without alignments)
2849.047 Million cell updates/sec

Title: US-09-367-052-2
Perfect score: 1867
Sequence: 1 MPEISVIYTSNDYSEVGS.....KRGCHSSVTESESSSFHSS 359

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US09367052/runat_10012006_102843_10231/app_query.fasta_1.519
-DB=Published Applications NA Main -OFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09367052 @CGN 1 1 1026 @runat_10012006_102843_10231 -NCFU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1867	100.0	1758	8	US-10-785-230-4
2	1744.5	93.4	1050	9	US-10-486-706-54
3	1678.5	89.9	1059	3	US-09-813-651B-84
4	1678.5	89.9	1059	6	US-10-014-322A-125
5	1678.5	89.9	1059	6	US-10-160-401-2
6	1678.5	89.9	1059	8	US-10-775-920-375
7	1678.5	89.9	1059	9	US-10-929-182-8
					Sequence 4, Appli
					Sequence 54, Appl
					Sequence 84, Appl
					Sequence 125, App
					Sequence 2, Appli
					Sequence 375, App
					Sequence 8, Appli

Alignment Scores: 1.12e-196 Length: 1758
Pred. No.: 1867.00 Matches: 359
Score:

ALIGNMENTS

RESULT 1
US-10-785-230-4
; Sequence 4, Application US/10785230
; Publication No. US20040209837A1
; GENERAL INFORMATION:
; APPLICANT: KISHIMOTO, Tadamitsu
; APPLICANT: NAGASAWA, Takashi
; APPLICANT: TACHIBANA, Kazunobu
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: Vascularization Inhibitors
; FILE REFERENCE: 46124-5042-US
; CURRENT APPLICATION NUMBER: US/10/785,230
; PRIOR FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: PCT/JP99/01448
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: JP10/95448
; PRIOR FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Mus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1080)
; OTHER INFORMATION:
US-10-785-230-4

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Sequence 741, App
Sequence 1235, Ap
Sequence 370, App
Sequence 2, Appli
Sequence 372, App
Sequence 374, App
Sequence 185, App
Sequence 11, Appl
Sequence 1213, Ap
Sequence 369, App
Sequence 2143, Ap
Sequence 636, App
Sequence 1, Appli
Sequence 77, Appl
Sequence 317, App
Sequence 367, App
Sequence 14, Appl
Sequence 75, Appl
Sequence 58, Appl
Sequence 312, App
Sequence 177, App
Sequence 80, Appl
Sequence 9, Appli
Sequence 912, App
Sequence 366, App
Sequence 64, Appl
Sequence 578, App
Sequence 62, Appl
Sequence 19, Appl
Sequence 373, App
Sequence 20, Appl
Sequence 459, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 5773, Ap
Sequence 484, App

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0
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QY	1	MetGluProPheSerValSerLeuThrLeuThrSerAspAsnTyrSerGluGluValGlySer	20
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QY	21	GlyAspTyrAspSerAsnLysGluProCysPheArgAspGluAsnValHisPheAsnArg	40
DB	61	GGAGACTATGACTCCCAACAAGGAACCTGCTCCGGGATGAAACCTGCCATTCATATAGG	120
QY	41	IlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyLeuValGlyAsnGlyLeu	60
DB	121	ATCTTCTGCCACCATCTACTTTCATCATCTTCTGACTGGCATAGTCGGCAATGGATTG	180
QY	61	ValIleLeuValMetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu	80
DB	181	GTGATCCTGCTCATGGTGTACCAAGAAGAGCTAAGGAGCATGACGACAAAGTACCGGCTG	240
QY	81	HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAla	100
DB	241	CACCTGTGAGTGGCTGACCTCTCTTGTTCATCACACTCCCTTCTGGGAGTGTATGCC	300
QY	101	MetAlaAspTrpTyrPheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrVal	120
DB	301	ATGGCTGACTGGTACTTGGGAATTTTGTGTGAAGGCTGTCCATATCATCTACACTGTC	360
QY	121	AsnLeuTyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIle	140
DB	361	AACCTCTAGACGAGGCTTCTATCTGGCCCTTCATGAGCTGGACCGTACCTCGGCAT	420
QY	141	ValHisAlaThrAsnSerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrVal	160
DB	421	GTCCAGCCCAACCAAGTCAAAGGCCAAGAACTGCTGCTGAAAGGCGAGTCTATGTG	480
QY	161	GlyValTrpIleProAlaLeuLeuThrIleProAspPheIlePheAlaAspValSer	180
DB	481	GGCGTCTGGATCCAGCCCTCTCTGACTATATACCTGACTTTCATCTTGTCCGACGTGAGC	540
QY	181	GlnGlyAspIleSerGlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSer	200
DB	541	CAGGGGACATCATAGTCAGGGGATGACAGGTATCTGTGACCGCTTTTACCCCGATAGC	600
QY	201	LeuTrpMetValValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIle	220
DB	601	CTGTGGATGGTGTGTTTCAATTCAGCATATATATGTTGGTCTCATCTCTCCCGGCATC	660
QY	221	ValIleLeuSerCysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln	240
DB	661	GTATCTCTCTCTTACTGCATCATCATCTCTAAAGCTGTACACATCCCAAGGGCCACAG	720
QY	241	LysArgLysAlaLeuLysThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeu	260
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QY	261	ProTyrTyrValGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGly	280
DB	781	CCATATATGTGGGGATCAGATCGACTCTCTTCATCTCTTGGGAGTCATCAAGCAAGGA	840
QY	281	CysAspPheGluSerIleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePhe	300
DB	841	TGTGACTTCGAGACATGTGTGCAAGTGGATCTCCATCACAGAGGCCCTCGCCTTCTTC	900
QY	301	HisCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAla	320
DB	901	CAGTGTGCTGAAACCCATCTCTATGCTTCTCGGGGCCAAGTTCAAAGCTCTGCCC	960
QY	321	GlnHisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLys	340
DB			

RESULT 2

US-10-486-706-54
 ; Sequence 54, Application US/10486706
 ; Publication No. US20050071088A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LANDFIELD, PHILIP W.
 ; APPLICANT: BLALOCK, ERIC M.
 ; APPLICANT: CHEN, KUEY-CHU
 ; APPLICANT: FOSTER, THOMAS C.
 ; TITLE OF INVENTION: GENE EXPRESSION PROFILE BIOMARKERS AND THERAPEUTIC TARGETS FOR
 ; TITLE OF INVENTION: BRAIN AGING AND AGE-RELATED COGNITIVE IMPAIRMENT
 ; FILE REFERENCE: 50229-426
 ; CURRENT APPLICATION NUMBER: US/10/486,706
 ; PRIOR FILING DATE: 2004-02-13
 ; PRIOR APPLICATION NUMBER: PCT/US02/25607
 ; PRIOR FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: US 60/311,343
 ; PRIOR FILING DATE: 2001-08-13
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 54
 ; LENGTH: 1050
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-10-486-706-54

Alignment Scores:
 Pred. No.: 2,16e-183 Length: 1050
 Score: 1744.50 Matches: 338
 Percent Similarity: 96.61% Conservative: 4
 Best Local Similarity: 95.48% Mismatches: 7
 Query Match: 93.44% Indels: 5
 DB: 9 Gaps: 1

US-09-367-052-2 (1-359) x US-10-486-706-54 (1-1050)

QY	6	ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer	25
DB	1	ATGGAATATATACACTTCGGATAACTACTCCGAAGAAGTAGGGTCTGGAGACTATGACTCC	60
QY	26	AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr	45
DB	61	AACAAGGAACCCCTGCTTCGGGATGAAACGAAACTTCAACAGGATCTTCTGCGCCACC	120
QY	46	IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet	65
DB	121	ATCTATTTATCATCTTCTGACTGGCATAGTGGGCATGGGTGGTGGTATCTCTGGTCATG	180
QY	66	GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla	85
DB	181	GGTTACCAGAAGAGCTGAGGAGCATGACAGACAGTACCGGCTGCACCTGTCCGTGGCT	240
QY	86	AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr	105
DB	241	GACCTCTCTTGTGTCATCATCTCCCTTCTGGGAGTGGACGCCATGGCTGACTGGTAC	300
QY	106	PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer	125
DB	301	TTTGGGAATTTTATGTAAGGCTGTGCATATCATCTACACCGTCAACCTTTACAGCAGT	360
QY	126	ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn	145
DB	361	GTCTCATCTCGGCTTCATGAGCTGGACCGCTACTCTTGCCATTTGCCACGCCCAAC	420
QY	146	SerGlnArgProArgLysLeuLeuAlaGlyAlaValTyrValGlyValTyrIlePro	165
DB	421	AGCCAGAGCGCGAAGGCTGCTGGCTGAAAGGCCGCTCTATGTGGGTGTCTGATCCCC	480

Qy	166	AlaLeuLeuLeuThrIleProAspPheIlePheAlaaspValSerGlnGlyAspIleSer	185
Db	481	GCCCTCCTCTGACTATCCCTGACATCATCTTCGCCGATGTC-----AGC	525
Qy	186	GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValVal	205
Db	526	CAGGGGACGGCAGGTATCATCTGTGACCGCGCTTTACCCCGACACCCCTGTGGATCGTGGTG	585
Qy	206	PheGlnPheGlnHisIleMetValGlyLeuLeuProGlyIleValIleLeuSerCys	225
Db	586	TTCCAGTTTCAGACACATCATGTGGTGGTCTCATCTCGCGGCATCGTCATCTCTCTCTGT	645
Qy	226	TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu	245
Db	646	TACTGCATCATCTCCAGCTGTACACTCCAAAGGGCCACCAAGAGCGCAAGGCCCTC	705
Qy	246	LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly	265
Db	706	AAGACTACGGTCACTCTATCTCGCTTTCTTTGGCTTGTGGCTACCGTATTACGTGGG	765
Qy	266	IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAppPheGluSer	285
Db	766	ATCAGCATCGATTCTCTTCATCCCTTTTGGAGGTCTATCAAGCAAGATGTGATTCGAGAGC	825
Qy	286	IleValHisLysTrpIleSerIleThrGluAlaIleuAlaPhePheHisCysCysLeuAsn	305
Db	826	GTTCGTGCAAGTGGATCTCATCACGGAGCCCTCGCCCTTCTTCCACTGTGTGCTCGAAC	885
Qy	306	ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn	325
Db	886	CCCATCTCTACGCTTCTCTCGGGCCCAATTCAGAGCTCCGGCGCAGCATGCATCTCAAT	945
Qy	326	SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer	345
Db	946	TCCATGACGAGAGGCTCCAGCTCAAGATCTTTTCCAAAGGAAACGGGGTGGACACTCT	1005
Qy	346	SerValSerThrGluSerGluSerSerPheHisSerSer	359
Db	1006	TCCGTCTCCAGAGTCAGATCTCTCAAGTTTTCACCTCCAGC	1047

QY 326 SerMetSerArgGlySerSerLeuLysLeuSerLysGlyLysArgGlyGlyHisSer 345
 DB 955 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCTCTCCANAGGAAGCGAGGTGGACATTCA 1014
 QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
 DB 1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1056

RESULT 4
 US-10-014-322A-125
 ; Sequence 125, Application US/10014322A
 ; Publication No. US20030167129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neetor, Jr., John
 ; APPLICANT: Wilson, Carol
 ; APPLICANT: Tan Hehir, Christina
 ; APPLICANT: Kates, Steven
 ; APPLICANT: Krstenansky, John
 ; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
 ; FILE REFERENCE: CNS-008
 ; CURRENT APPLICATION NUMBER: US/10/014,322A
 ; CURRENT FILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: US 60/243,587
 ; PRIOR FILING DATE: 2000-10-27
 ; PRIOR APPLICATION NUMBER: US 09/813,651
 ; PRIOR FILING DATE: 2001-03-20
 ; PRIOR APPLICATION NUMBER: US 09/813,653
 ; PRIOR FILING DATE: 2001-03-20
 ; PRIOR APPLICATION NUMBER: US 09/813,448
 ; PRIOR FILING DATE: 2001-03-20
 ; NUMBER OF SEQ ID NOS: 126
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 125
 ; LENGTH: 1059
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1059)
 ; OTHER INFORMATION: human CXCR4 gene
 US-10-014-322A-125

Alignment Scores:
 Pred. No.: 4 81e-176 Length: 1059
 Score: 1678.50 Matches: 319
 Percent Similarity: 95.48% Conservative: 19
 Best Local Similarity: 90.11% Mismatches: 11
 Query Match: 89.90% Indels: 5
 DB: 6 Gaps: 1

US-09-367-052-2 (1-359) x US-10-014-322A-125 (1-1059)

QY 6 ValSerIleThrSerAspAsnThrSerGluValGlySerGlyAspThrAspSer 25
 DB 10 ATCAGTATATACACTTCAGATACTACACCGAGGAATGGCTCAGGGAGTATGACTCC 69
 QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
 DB 70 ATGAAGGAACCCCTGTTTCCGTGAAGAAATGCTAAATTTCAATAAAATCTTCTCCGCCCCACC 129
 QY 46 IleThrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
 DB 130 ATCTACTCCATCACTCTTAACTGGCATTTGGGCNATGGATGGTTCATCTCGTTCATG 199
 QY 66 GlyThrGlnLysLysLeuArgSerMetThrAspLysThrArgLeuHisLeuSerValAla 85
 DB 190 GGTACCAAGAAATCTGAGAAGCATGACCGCATGACAGGTACAGGCTGCACCTGTGAGTGCC 249
 QY 86 AspLeuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspThrThr 105
 DB 250 GACCTCTCTTGTTCATCAGCTTCCCTTCTGGCAGTTCATGCCGTGGCAAACTGGTAC 309
 QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleThrValAlaLeuLeuThrSerSer 125

DB 310 TTTGGGAACCTTCTTATGCAAGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT 369
 QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgThrLeuAlaIleValHisAlaThrAsn 145
 DB 370 GTCCCTCATCTGGCCTTTCATCAGTCTGGACCCCTACCTGGCCATCGTCCACGCCCAAC 429
 QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValThrValGlyValTrpIlePro 165
 DB 430 AGTCAGAGCCCAAGGAGCTGTGGCTGAAAGGTGCTATGTTGGCCTCTGGATCCCT 489
 QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
 DB 490 GCCCTCTCTGCTGACTATTCCCGACTTCATCTTTGCCAAGCTC-----AGT 534
 QY 186 GlnGlyAspAspArgThrIleCysAspArgLeuThrProAspSerLeuTrpMetValVal 205
 DB 535 GAGGCAGATGACAGATATATCTGTGACCCCTTCTACCCCAATGACTGTGGGTGTGTG 594
 QY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225
 DB 595 TTCCAGTTTCAGCACATCATGTTGGCTTATCTTCGCTGTGATGTTGTCATCTCTGCTGC 654
 QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
 DB 655 TATTGCATTATCATCTCCAAGCTGTCCACTCCAAGGGCCACCCAGAAAGCGCAAGGCCCTC 714
 QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysThrLeuProThrThrValGly 265
 DB 715 AAGACCACAGTTCATCTCTGCTTCTTCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 774
 QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
 DB 775 ATCAGCATCGACTCTCTTCTCTCTGGAATCATCAACAGGGTGTGAGTTTGAGAAC 834
 QY 286 IleValHisLysThrIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
 DB 835 ACTGTGCACAGTGGATTTCCATCACCAGGGCCCTAGCTTTCTTCCACTGTTGCTCTGAAC 894
 QY 306 ProIleLeuThrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
 DB 895 CCCATCTCTATGCTTCTCTGGAGCAAAATTTAAACCTCTGCCCGACGACGACTCACC 954
 QY 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
 DB 955 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCTCTCCANAGGAAGCGAGGTGGACATTCA 1014
 QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
 DB 1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1056

RESULT 5
 US-10-160-401-2
 ; Sequence 2, Application US/10160401
 ; Publication No. US20030207281A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genaisance Pharmaceuticals, Inc.
 ; APPLICANT: Bentivegna, Steven C.
 ; APPLICANT: Bieglecki, Karyn M.
 ; APPLICANT: Koshiy, Beena
 ; APPLICANT: Monroe, Glen
 ; APPLICANT: Rounds, Eileen
 ; TITLE OF INVENTION: HAPLOTYPES OF THE CXCR4 GENE
 ; FILE REFERENCE: MWH-0121US
 ; CURRENT APPLICATION NUMBER: US/10/160,401
 ; CURRENT FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: PCT/US01/12268
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: US 60/197,025
 ; PRIOR FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2

```
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-160-401-2

Alignment Scores:
Pred. No.: 4,81e-176 Length: 1059
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 1 Gaps: 1

US-09-367-052-2 (1-359) x US-10-160-401-2 (1-1059)

Qy 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 10 ATCAGTATATACACTTCAGATAACTACACCGAGAAATGGCTCAGGGGACTATGACTCC 69

Qy 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 70 ATGAAGGAAACCTGTTTCCGTAAGAAAAATGCTAAATTTCAATAAAATCTTCTGCCACC 129

Qy 46 IleTyrPheIleIlePheLeuThrGlyValGlyAsnGlyLeuValIleLeuValMet 65
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 130 ATTACTCCATCATCTCTTTAACTGGCAATTTGGGCAATGGATTTGGTTCATCTGGTCATG 189

Qy 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 190 GGTACCAGAAAGAACTGAGAACATGACGACAGATGACAGGCTGCACCTGTCTAGTGGCC 249

Qy 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTyrTyr 105
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 250 GACCTCTCTTCTGTCATCAGCTTCCTCTTGGGCAATTTGATGCGGCAAACTGGTAC 309

Qy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 310 TTTGGGAACCTTCTTATGCAAGGCGAGTCCATGTCTATCATCAGTCAACCTCTACAGCAGT 369

Qy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 370 GTCTCATCTGCGCTTTCATCAGTCTGGACCGCTACCTGGCCATCTGTCACGCCACCAC 429

RESULT 6
US-10-775-920-375
; Sequence 375, Application US/10775920
; Publication No. US20040175744A1
; GENERAL INFORMATION:
; APPLICANT: Mergen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; FILE REFERENCE: Merzen - 00108
; CURRENT APPLICATION NUMBER: US/10/775,920
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 375
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-920-375

Alignment Scores:
Pred. No.: 4,81e-176 Length: 1059
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 1 Gaps: 1

US-09-367-052-2 (1-359) x US-10-775-920-375 (1-1059)

Qy 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 10 ATCAGTATATACACTTCAGATAACTACACCGAGAAATGGCTCAGGGGACTATGACTCC 69

Qy 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 70 ATGAAGGAAACCTGTTTCCGTAAGAAAAATGCTAAATTTCAATAAAATCTTCTGCCACC 129

Qy 46 IleTyrPheIleIlePheLeuThrGlyValGlyAsnGlyLeuValIleLeuValMet 65
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 130 ATTACTCCATCATCTCTTTAACTGGCAATTTGGGCAATGGATTTGGTTCATCTGGTCATG 189

Qy 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 190 GGTACCAGAAAGAACTGAGAACATGACGACAGATGACAGGCTGCACCTGTCTAGTGGCC 249

Qy 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTyrTyr 105
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 250 GACCTCTCTTCTGTCATCAGCTTCCTCTTGGGCAATTTGATGCGGCAAACTGGTAC 309

Qy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 310 TTTGGGAACCTTCTTATGCAAGGCGAGTCCATGTCTATCATCAGTCAACCTCTACAGCAGT 369

Qy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 370 GTCTCATCTGCGCTTTCATCAGTCTGGACCGCTACCTGGCCATCTGTCACGCCACCAC 429
```

146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrrpIlePro 165
147 |||||
430 AGTCAGAGGCCAAGAGCTGTTGGCTGAAAGGTGTCTATGTTGGCTGTGATCCCT 489
166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
167 |||||
490 GCCCTCTGCTGACTATTCGCGACTTCATCTTTGCCAACGTC-----AGT 534
186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrrpMetValVal 205
187 ::::|
535 GAGGCAGATGACAGATATATCTGTGACCGCTTACCCCAATGACTTGTGGTGTGTG 594
206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225
207 |||||
595 TTCAGTTTCAGACATCATGTTGGCTTATCTGCTGGTATTTGTCATCTGTCTGTC 654
226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysAlaLeu 245
227 |||||
655 TATTGCAATTATCATCTCCAAGCTGTACACTCCAGGGCCACCAGAGCGCAAGGCCCTC 714
246 LysThrThrValIleLeuLeuAlaPhePheAlaCysTrrpIleuProTyrTrrpValGly 265
247 |||||
715 AAGACCACAGTCATCTCATCTGCTGCTTCTCGCTGTTGGCTGTGCTTACTACATTGGG 774
266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
267 |||||
775 ATCAGATGACCTCTTCATCTCTCTGGAATCATCAAGAGGGTGTGATTTGAGAAC 834
286 IleValHisLysTrrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
287 |||||
835 ACTGTGCACAAAGTGGATTTCCATCACCGAGGCCCTAGCTTCTTCCACTGTTGCTGAAC 894
306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
307 |||||
895 CCCATCTCTATGCTTCTCTTGGAGCCAAATTTAAACCTCTGCCAGCAGCACTCACC 954
326 SerMetSerArgGlySerSerLeuLeuValIleLeuSerLysGlyLysArgGlyGlyHisSer 345
327 |||||
955 TCTGTGAGCAGAGGGTCCAGCTCAAGATCTCTCCAAAGAAAGGAGGTGGACATTCA 1014
346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1056

RESULT 7

US-10-929-182-8
; Sequence 8, Application US/10929182
; Publication No. US20050064483A1
; GENERAL INFORMATION:
; APPLICANT: Zang, Jingwu
; APPLICANT: Hong, Jian
; TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of
; TITLE OF INVENTION: Multiple Sclerosis
; FILE REFERENCE: HO-P02859US1
; CURRENT APPLICATION NUMBER: US/10/929,182
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,731
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: HUMAN
US-10-929-182-8

Alignment Scores:

Pred. No.:	4,81e-176	Length:	1059
Score:	1678.50	Matches:	319
Percent Similarity:	95.48%	Conservative:	19
Best Local Similarity:	90.11%	Mismatches:	11
Query Match:	89.90%	Indels:	5

DB: 9 Gaps: 1

US-09-367-052-2 (1-359) x US-10-929-182-8 (1-1059)

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
26 ::::|
DB 10 ATCAGTATATACACTTCAGATAACTACACCGAGGAATGGCTCAGGGGACTATGACTCC 69
QY 26 AsnLysGluProCysPheArgPheGluAsnValHisPheAsnArgIlePheLeuProThr 45
27 ::::|
DB 70 ATGAAGAAACCTGTTTCCGTGAAGAAATGCTAATTTCAATAAAATCTTCCTGCCACC 129
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
47 |||||
DB 130 ATCTACTCCATCATCTTCTTAAGTGGCATTTGGGCAATGGATTGCTCATCTCGTGGTCATG 189
QY 66 GlyTyrGlnLysLeuArgSerMetThrAspLysTyrArgLeuHisIleuSerValAla 85
67 |||||
DB 190 GGTTACCAGAAAGAACTGAGAAAGCATGACGACAGTACAGGCTGCACCTGTCAAGTGGCC 249
QY 86 AspLeuLeuPheValIleThrLeuProPheTrrpAlaValAspAlaMetAlaAspTrrpTyr 105
87 |||||
DB 250 GACCTCTCTTGTTCATCAGCTTCCCTTCTGGGAGTTGATGCCGTGGCAAACTGGTAC 309
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
107 |||||
DB 310 TTTGGGAACCTTCTATGCAAGGAGTCCATGTCATCTACACAGTCAACCTCTACACAGCT 369
QY 126 ValLeuIleAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
127 |||||
DB 370 GTCTCTCATCTGCGCTTCATGTCAGTGGACCGCTACCTGCCCATCTGCACGCCACCAAC 429
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrrpIlePro 165
147 |||||
DB 430 AGTCAGAGGCCAAGAGCTGTTGGCTGAAAGGTGTCTATGTTGGCTGTGATCCCT 489
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
167 |||||
DB 490 GCCCTCTCTGCTGACTATTTCCGACTTTCATCTTTGCCAACGTC-----AGT 534
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrrpMetValVal 205
187 ::::|
DB 535 GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGTGTGTG 594
QY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225
207 |||||
DB 595 TTCAGTTTCAGACATCATGTTGGCTTATCTGCTGGTATTTGTCATCTGTCTGTC 654
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysAlaLeu 245
227 |||||
DB 655 TATTGCAATTATCATCTCCAAGCTGTACACTCCAGGGCCACCAGAGCGCAAGGCCCTC 714
QY 246 LysThrThrValIleLeuLeuAlaPhePheAlaCysTrrpIleuProTyrTrrpValGly 265
247 |||||
DB 715 AAGACCACAGTCATCTCATCTGCTGCTTCTCGCTGTTGGCTGTGCTTACTACATTGGG 774
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
267 |||||
DB 775 ATCAGATGACCTCTTCATCTCTCTGGAATCATCAAGAGGGTGTGATTTGAGAAC 834
QY 286 IleValHisLysTrrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
287 |||||
DB 835 ACTGTGCACAAAGTGGATTTCCATCACCGAGGCCCTAGCTTCTTCCACTGTTGCTGAAC 894
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
307 |||||
DB 895 CCCATCTCTATGCTTCTCTTGGAGCCAAATTTAAACCTCTGCCAGCAGCACTCACC 954
QY 326 SerMetSerArgGlySerSerLeuLeuValIleLeuSerLysGlyLysArgGlyGlyHisSer 345
327 |||||
DB 955 TCTGTGAGCAGAGGGTCCAGCTCAAGATCTCTCCAAAGAAAGGAGGTGGACATTCA 1014
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359

Db 1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1056
|||||

RESULT 8

US-10-985-324-1
; Sequence 1, Application US/10985324
; Publication No. US20050202019A1
; GENERAL INFORMATION:
; APPLICANT: Northwest Biotherapeutics, Inc.
; APPLICANT: Murphy, Gerald P.
; APPLICANT: Boynton, Alton L.
; APPLICANT: Sehgal, Anil
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED ON THE
; FILE OF INVENTION: ROLE OF THE CXCR-4 GENE IN TUMORIGENESIS
; FILE REFERENCE: 20093-000600PC
; CURRENT FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US/09/647,501
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/079,916
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/104,656
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-985-324-1

Alignment Scores:

Pred. No.: 4,91e-176 Length: 1059
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 9 Gaps: 1

US-09-367-052-2 (1-359) x US-10-985-324-1 (1-1059)

QY 6 ValSerIleThrSerAspPheLeuValGlySerGlyAspTyrAspSer 25
Db 10 ATCAGTATATACACTTCCAGATACTACACGAGAAATGGCTCAGGGGACTATGACTCC 69
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 70 ATGAGGAACCTGTTTCCGTGAGAAATGCTAATTTCAATAAATCTTCTGCCCCACC 129
QY 46 IleTyrPheIlelePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 130 ATCTACTCCATCATCTTCTTAACTGGCATTTGGCAATGGATTGGTTCATCTGGTCATG 189
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 190 GGTTCACAGAAGAACTGAGAAGCATGACGACGACGATGACAGGCTGCACCTGTGAGTGGCC 249
QY 86 AspLeuLeuPheValIleThrLeuPropheTyrAlaValAspAlaMetAlaAspTyrTyr 105
Db 250 GACCTCTCTTTGTATCAGCTTCCCTTCTGGCAGTTGATGCGGTGGCAAACTGGTAC 309
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 310 TTTGGGAACCTTCATGCAAGGCGAGTCCATGTCTACACAGTCAACCTCTACAGCAGT 369
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 370 GTCTCTATCTGCGCTTCATCATGCTGGACCGTACTCGGCCATCGTCCACGCGCAAC 429
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrIlePro 165
Db 430 AGTCAGAGGCGCAAGGAAGCTGTTGGCTGTAAGAGGTGGTCTATGTTGGCGTCTGGATCCCT 489

QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 490 GCCCTCTCTGCTGACTATTCCGACTTTCATCTTTGCCAACGTC-----AGT 534
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValVal 205
Db 535 GAGCGAGATGACAGATATATCTGTGACCGCTTACCCCAATGACTTGTGGGTGTGTG 594
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 595 TTCAGTTTTCAGCACATCATGTTGGCTTATCTGCTGCTGTTATGTCATCTGCTCTGC 654
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 655 TATTGCAATTATCATCTCCAAGCTGTCCACTCCAAGGGCCACCAGAACGCAAGGCCCTC 714
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
Db 715 AAGACCACAGTCATCTCTGCTGCTTCTTCCGCTGTTGGCTGCTTACTACTACTGGG 774
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 775 ATCAGCATCGACTCTCTCATCTCTCGAAATCATCAAGCAAGGCTGTGAGTTGAGAAC 834
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 835 ACTGTGCACAAAGTGGATTTCATCAGCGAGGCTAGCTTTCTTCCACTGTGTGCTGAAC 894
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 895 CCATCTCTATGCTTCTCTTGGAGCAAAATTTAAACCTCTGCCAGCAGCACTCACC 954
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
Db 955 TCTGTGAGCAGAGGGTCCAGCTCAAGATCTCTCCAAAGGAAGGAGGTGGACATTCA 1014
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1056

RESULT 9
US-10-101-510-741
; Sequence 741, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WANG, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 741
; LENGTH: 1225
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-741

Alignment Scores:
Pred. No.: 6.02e-176 Length: 1225
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 6 Gaps: 1

US-09-367-052-2 (1-359) x US-10-101-510-741 (1-1225)

QY 6 ValSerIleThrSerAspPheLeuValGlySerGlyAspTyrAspSer 25
Db 1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1056

35 ATCAGTATATACACTTCAGATAACTACACCGAGGAAATGGCTCAGGGGACTATGACTCC 94
 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
 95 ATGAAGGAACCTGTTTCCGTGAAGAAATGCTAAATTTCAATAAAATCTTCCTGCCACC 154
 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
 155 ATCTACTCCATCATCTCTTAACCTGGCATTTGGGCAATGGATGGTTCATCCTGGTCATG 214
 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
 215 GGTTACCAGAAGAACTGAGAAGCATGACGACAGTACAGGCTGCACCTGTCACTGGCC 274
 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
 275 GACCTCTCTTGTCTATCAGCTTCCTCTTGGGCAATGATCCGCTGGCAAACTGGTAC 334
 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
 335 TTGGGAACCTCTCTATGCAAGGAGTCCATGTCTATCACAGCTCAACCTCTACAGAGT 394
 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
 395 GTCTCTCATCTGGCCTTCATCAGTCTGGACCGTACCTGGCCATCGTCCACGCCCAAC 454
 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
 455 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAGAGGTGCTCTATGTTGGCGTCTGGATCC 514
 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
 515 GCCTCTCTGTGACTATATCCGACTTCATCTTTGCCAACGTC-----AGT 559
 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
 560 GAGGCAGATGACAGATATATCTGTGACCGCTCTACCCCAATGACTTGTGGGTGGTTGTG 619
 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
 620 TTCCAGTTTCAGCACATCATCTGTCGCTTATCTGCTGCTGATTTGTCATCTGCTGCTGC 679
 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
 680 TATGTATATATCATCTCCAGCTGTCTACATCTCAAGGCCCAAGAGCCCAAGGCCCTC 739
 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
 740 AAGACCACAGTATCTCTATCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 799
 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
 800 ATCAGCATCGACTCTCTATCTCTCTGGAATCATCAAGCAAGGGGTGTGAGTTTGAAC 859
 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysLysLeuAsn 305
 860 ACTGTGCACAAAGTGAATTTCCATCACCAGGCCCTAGCTTCTTCCACTGTGCTGTAAC 919
 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
 920 CCCATCTCTATGCTTCTTGTGGGCCAAATTTAAACCTCTGCCAGCAGCACCTCACC 979
 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
 980 TCTGTGAGCAGAGGGTCCAGCTCAAGATCTCTCCAAAGAAAGCGAGGTGGACATTC 1039
 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
 1040 TCTGTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1081

RESULT 10
 US-10-305-720-1235
 ; Sequence 1235, Application US/10305720

; Publication No. US20040010136A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
 ; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
 ; FILE REFERENCE: PA-0002-1 CON
 ; CURRENT APPLICATION NUMBER: US/10/305,720
 ; CURRENT FILING DATE: 2002-11-26
 ; PRIOR APPLICATION NUMBER: 09/016,434
 ; PRIOR FILING DATE: 1998-01-30
 ; NUMBER OF SEQ ID NOS: 1490
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1235
 ; LENGTH: 1225
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: GenBank ID No. US20040010136A1 g189313
 ; US-10-305-720-1235
 Alignment Scores:
 Pred. No.: 6,02e-176 Length: 1225
 Score: 1678.50 Matches: 319
 Percent Similarity: 95.48% Conservative: 19
 Best Local Similarity: 90.11% Mismatches: 11
 Query Match: 89.90% Indels: 5
 DB: 6 Gaps: 1
 US-09-367-052-2 (1-359) x US-10-305-720-1235 (1-1225)
 QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
 DB 35 ATCAGTATATACACTTCAGATAACTACACCGAGGAAATGGCTCAGGGGACTATGACTCC 94
 QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
 DB 95 ATGAAGGAACCTGTTTCCGTGAAGAAATGCTAAATTTCAATAAAATCTTCCTGCCACC 154
 QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
 DB 155 ATCTACTCCATCATCTCTTAACCTGGCATTTGGGCAATGGATGGTTCATCCTGGTCATG 214
 QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
 DB 215 GGTTACCAGAAGAACTGAGAAGCATGACGACAGTACAGGCTGCACCTGTCACTGGCC 274
 QY 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
 DB 275 GACCTCTCTTGTCTATCAGCTTCCTCTTGGGCAATGATCCGCTGGCAAACTGGTAC 334
 QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
 DB 335 TTGGGAACCTCTCTATGCAAGGAGTCCATGTCTATCACAGCTCAACCTCTACAGAGT 394
 QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
 DB 395 GTCTCTCATCTGGCCTTCATCAGTCTGGACCGTACCTGGCCATCGTCCACGCCCAAC 454
 QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
 DB 455 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAGAGGTGCTCTATGTTGGCGTCTGGATCC 514
 QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
 DB 515 GCCTCTCTGTGACTATATCCGACTTCATCTTTGCCAACGTC-----AGT 559
 QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
 DB 560 GAGGCAGATGACAGATATATCTGTGACCGCTCTACCCCAATGACTTGTGGGTGGTTGTG 619
 QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
 DB 620 TTCCAGTTTCAGCACATCATCTGTCGCTTATCTGCTGCTGATTTGTCATCTGCTGCTGC 679


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; PRIOR APPLICATION NUMBER: PCT/J999/01448
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: JP10/95448
; PRIOR FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Mus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (1059)
US-10-785-230-2

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Alignment Scores:		
Pred. No.:	8.97e-176	Length:
Score:	1678.50	Matches:
Percent Similarity:	95.48%	Conservative:
Best Local Similarity:	90.11%	Mismatches:
Query Match:	89.90%	Indels:
DB:	8	Gaps:
		1
		5
		11
		19
		319
		1588

US-09-367-052-2 (1-359) x US-10-785-230-2 (1-1588)

Qy	6	ValSerIleTyrThrSerAspAsnTyrSerGluGluValValGlySerGlyAspTyrAspSer	25
Db	10	ATCAGTATATACACATTCAGATAACTACACCGAGAAATGGGCTCAGGGGACTATGACTCC	69
Qy	26	AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr	45
Db	70	ATGAAGGAACCCCTGTTCCGTAAGAAATAATGCTAATTCAATAAATAATTCCTCGGCCACCC	129
Qy	46	IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet	65
Db	130	ATCTACTCCATCATCTTCTTAACTGGCATTTGTGGGCAATGGATTGGTCATCCTGGTCATG	189
Qy	66	GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla	85
Db	190	CGTTACCAGAAACTCAGAAGCATGACGACAGAAGTACAGGCTGCACCTGTCACTGGCC	249
Qy	86	AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr	105
Db	250	GACCTCCCTTTGTTCATCACGCTTCCCTTCTGGGCAGTTGATGCGCGGCAAACTGGTAC	309
Qy	106	PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer	125
Db	310	TTTGGGAACCTTCCTATGACGAGCAGTCATGTCATCTACAGTCAACCTCTCAGCAGT	369
Qy	126	ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn	145
Db	370	GTCCCTCATCCTGGCCTTCATCAGTCTGACCGCTACCTGGCCATCGTCCACGCCACCAAC	429
Qy	146	SerGlnArgProArgLysIleuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro	165
Db	430	AGTCAGAGCCCAAGGAAGCTGTTGGCTGAAAGGTGGTCTATGTTGGCGCTCGGATCCCT	489
Qy	166	AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer	185
Db	490	GGCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAACGTC-----AGT	534
Qy	186	GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal	205
Db	535	GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGGTGTG	594
Qy	206	PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys	225
Db	595	TTCCAGTTTCAGCACATCATGTTGGCCCTTATCTTCGCTGGTATTGTTCATCCTGTCTGC	654
Qy	226	TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu	245
Db	655	TATTGCATTATCATCTCCAAGCTGTCACTCCCAAGGGGCCACCAAGACGCAAGGCCCTC	714
Qy	246	LysThrThrValIleLeuIleLeuAlaPheAlaCysTrpLeuProTyrTyrValGly	265

RESULT 13

US-10-775-920-372 ; Sequence 372, Application US/10775920
; Publication No. US20040175744A1

```

; GENERAL INFORMATION:
; APPLICANT: Mergen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; TITLE OF INVENTION: IN CERTAIN CANCERS
; FILE REFERENCE: Mergen - 0010B
; CURRENT APPLICATION NUMBER: US/10/775,920
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 372

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Alignment Scores:	9.4e-176	Length:	1637
Pred. No.:	1678.50	Matches:	319
Score:	95.48%	Conservative:	19
Percent Similarity:	90.11%	Mismatches:	11
Best Local Similarity:	89.90%	Indels:	5
Query Match:	8	Gaps:	1
DB:			

US-09-367-052-2 (1-359) x US-10-775-920-372 (1-1637)

Qy	6	ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer	25
Db	94	ATCAGTATATACACTTCAGATAACTACACCGAGAAATGGGCTCAGGGGACTATGACTCC	153
Qy	26	AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr	45
Db	154	ATGAGGAAACCTGTTCCTCGTGAAGAAATGCTAAATTTCAATAAATCTTCTCGCCACC	213
Qy	46	IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet	65
Db	214	ATCTACTCCATCATCTCTTAACCTGGCAATGTGGCAATGGATGGTCATCTCTGGTCATG	273
Qy	66	GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla	85
Db	274	GGTTACCGAAGAAACTCAGAAGCATGACGACACAAGTACAGGCTGCACCTGTCAAGTGCC	333
Qy	86	AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr	105

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Db 334 GACCTCTCTTTGTATCATCGCTTCCCTTCTGGCAGTTGATGCCGTGGCAAACTGGTAC 393
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 394 TTTGGGAACCTTCATGCAAGGCAGTCATGTATCATACAGTCACAGCTTCTACAGCAGT 453
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 454 GTCCCTCATCTGCGCTTCATCAGCTGGACCGTACCTGGCCCATCGTCCACGCCCAAC 513
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrPlePro 165
Db 514 AGTCAGAGGCCAAGAGCTGTGGCTGAAGAAGTGTGTATGTTGGCTGTGATCCCT 573
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 574 GCCCTCTCTGTGACTATTCCGACTTCATCTTTGCCAACGTC-----AGT 618
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
Db 619 GAGGCGAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGTG 678
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 679 TTCAGTTTCAGCACATCATCTGCTGGCTTATCTGCTCGTATGTCATCTGCTCTGTC 738
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 739 TATTGCATTATCATCTCCAGCTGTCCACTCCAGGGCCACCAGAGCGCAAGGCCCTC 798
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
Db 799 AAGACACACAGTCATCTCATCTGCTGCTTCTCGCTGCTGCTGCTTACTACATTGGG 858
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 859 ATCAGATCGACTCTCTTCATCTCTCGGAATCATCAAGCAAGGGTGTGATTGAGAAC 918
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 919 ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTCTCCACTGTTGCTGAAAC 978
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 979 CCCATCTCTATGCTTCTCTTGGAGCCAAATTTAAACCTCTGCCACGACGCACTCACC 1038
QY 326 SerMetSerArgGlySerSerLeuValIleLeuSerLysGlyLysArgGlyGlyHisSer 345
Db 1039 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCTCTCCAAAGAAAGCGAGGTGACATTCA 1098
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1099 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1140

RESULT 14
US-10-775-920-374
; Sequence 374, Application US/10775920
; Publication No. US2004017544A1
; GENERAL INFORMATION:
; APPLICANT: Mergen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; FILE REFERENCE: Mergen - 00108
; CURRENT APPLICATION NUMBER: US/10/775, 920
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447, 900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 374
; LENGTH: 1645
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-775-920-374
Alignment Scores:
Pred. No.: 9, 47e-176 Length: 1645
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
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Query Match: 89.90% Indels: 5
DB: 8 Gaps: 1

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Db 137 ATGAAGAAACCCCTGTTTCCGTGAAGAAATGCTAATTTCAATAAATCTTCTGCCACC 196
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
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QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 257 GGTATACAGAAAGAACTGAGAGAGCATGACGAGCAAGTACAGGCTGCACCTGTCTGAGTGGCC 316
QY 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
Db 317 GACCTCTCTTTGTATCATCGCTTCCCTTCTGGCAGTTGATGCCGTGGCAAACTGGTAC 376
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 377 TTTGGAACTTCTATGCAAGGCAGTCCATGTCTACACAGTCAACCTCTACAGCAGT 436
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 437 GTCTCTCATCTGCGCTTCTCATGCTGGACCGCTACCTGCGCATCTGCCCATCCACCAAC 496
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrPlePro 165
Db 497 AGTCAGAGCCCAAGGAAGCTGTGGCTGAAGAAGTGTGTATGTTGGCGTCTGATCCCT 556
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
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QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 662 TTTCCAGTTTCAGCACATCATGTTGGCTTATCTCTGCTGGTATGTCATCTCTGCTGCTG 721
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 722 TATTGCATTATCATCTCCAGCTGTCTCACTCCAGGGCCACCAGAGCGCAAGGGCCCTC 781
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
Db 782 AAGACCACAGTCTCATCTCTGCTTCTTCTGCTGCTTCTGCTGCTTCTTACTACTTGGG 841
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 Db 1022 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA 1081
 QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
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RESULT 15
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 ; Sequence 185, Application US/10505680
 ; Publication No. US2005009592A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Government of the United States of America as represented by the
 ; APPLICANT: Secretary of the Department of Health and Human Services
 ; APPLICANT: Jazaeri, Amir A.
 ; APPLICANT: Boyd, Jeff
 ; APPLICANT: Liu, Edison T.
 ; TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THERAPEUTIC TA
 ; FILE REFERENCE: 4239-64452
 ; CURRENT APPLICATION NUMBER: US/10/505,680
 ; CURRENT FILING DATE: 2004-08-12
 ; PRIOR APPLICATION NUMBER: 60/357,031
 ; PRIOR FILING DATE: 2002-02-13
 ; NUMBER OF SEQ ID NOS: 822
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 185
 ; LENGTH: 1645
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-505-680-185

Alignment Scores:
 Pred. No.: 9 47e-176 Length: 1645
 Score: 1678.50 Matches: 319
 Percent Similarity: 95.48% Conservative: 19
 Best Local Similarity: 90.11% Mismatches: 11
 Query Match: 89.90% Indels: 5
 DB: 9 Gaps: 1

US-09-367-052-2 (1-359) x US-10-505-680-185 (1-1645)

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
 Db 77 ATCAGTATATACACTTCAGATAACTACACCGAGGAAATGGCTCAGGGGACTATGACTCC 136
 QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
 Db 137 ATGAAGGAACCCCTGTTTCCGTGAAGAAATGCTAATTTCAATAAAATCTTCTCGCCACC 196
 QY 46 IleTyrPheIleIlePheLeuThrGlyValGlyAsnGlyLeuValIleLeuValMet 65
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 QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
 Db 257 GGTATCCAGAAAGAACTGAGAAGCATACGCGAATGACAGGTGACACCTGTGAGTGGCC 316
 QY 86 AspLeuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTyrTyr 105
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 Db 437 GTCTCTATCTGGCCTTTCATCAGTCTGGACGGCTTACCTGGCCCATCGTCCAGCCCAAC 496

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 QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
 Db 557 GCCCTCTCTGCTGACTATTCCCGACTTCATCTTTGCCAAGTC-----AGT 601
 QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValVal 205
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 QY 246 LysThrThrValIleLeuIleLeuAlaPheAlaCysThrLeuProTyrTyrValGly 265
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 QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
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Search completed: January 11, 2006, 02:44:21
 Job time : 1051 secs

GenCore version 5.1.6
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Run on: January 11, 2006, 00:27:42 ; Search time 257 Seconds
(without alignments)
1018.422 Million cell updates/sec

Title: US-09-367-052-2

Perfect score: 1867

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Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

Published Applications NA New:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1738.5	93.1	1651	7	Sequence 4, Appli
3	1678.5	89.9	1225	6	Sequence 2630, Ap
4	1678.5	89.9	1662	7	Sequence 112, App
5	1678.5	89.6	8747	6	Sequence 3, Appli
6	1670.5	89.5	1102	6	Sequence 141, App
7	1606	86.0	1643	7	Sequence 121, App
8	1320.5	70.7	1400	7	Sequence 108, App
					Sequence 6726, Ap

9	1268	67.9	1400	7	US-11-136-527-4204	Sequence 4204, Ap
10	594	31.8	1680	7	US-11-136-527-153	Sequence 153, App
11	576	30.9	1400	7	US-11-136-527-4249	Sequence 4249, Ap
12	562	30.1	1324	7	US-11-136-527-2373	Sequence 2373, Ap
13	540	28.9	3100	6	US-10-775-169-254	Sequence 254, App
14	535	28.7	3177	7	US-11-127-877-25	Sequence 25, Appl
15	533	28.5	30151	6	US-10-995-561-13239	Sequence 13239, A
16	531	28.4	3062	6	US-10-995-561-120	Sequence 120, App
17	531	28.4	3101	6	US-10-995-561-119	Sequence 119, App
18	522.5	28.0	246960	6	US-11-121-086-8	Sequence 8, Appli
19	510.5	27.3	1348	7	US-11-136-527-3311	Sequence 3311, A
20	508	27.2	1433	6	US-10-750-185-54253	Sequence 54253, A
21	508	27.2	1433	6	US-10-750-623-54253	Sequence 54253, A
22	498	26.7	2273	7	US-11-127-877-23	Sequence 23, Appl
23	494	26.5	1365	7	US-11-136-527-2610	Sequence 2610, Ap
24	493.5	26.4	1251	7	US-11-122-849-1	Sequence 1, Appli
25	492.5	26.4	1383	7	US-11-136-527-3271	Sequence 3271, Ap
26	484.5	26.0	1059	7	US-11-068-686-19	Sequence 19, Appl
27	483.5	25.9	3383	7	US-11-068-686-1	Sequence 1, Appli
28	483.5	25.9	3855	7	US-11-127-877-24	Sequence 24, Appl
29	477.5	25.6	1915	7	US-11-068-686-3	Sequence 3, Appli
30	477.5	25.6	1945	7	US-11-127-877-27	Sequence 27, Appl
31	471	25.2	1515	7	US-11-136-527-2563	Sequence 2563, Ap
32	464.5	24.9	2338	6	US-10-876-787-1	Sequence 1, Appli
33	463.5	24.8	2214	6	US-10-995-561-195	Sequence 195, App
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35	463.5	24.8	2347	7	US-11-127-877-28	Sequence 28, Appl
36	463.5	24.8	2363	6	US-10-995-561-197	Sequence 197, App
37	463.5	24.8	2422	6	US-10-995-561-195	Sequence 195, App
38	463.5	24.8	2480	6	US-10-995-561-198	Sequence 198, App
39	463.5	24.8	57198	6	US-10-995-561-13263	Sequence 13263, A
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41	463	24.8	2580	7	US-11-136-527-3525	Sequence 3525, Ap
42	462.5	24.8	1339	7	US-11-136-527-4061	Sequence 4061, Ap
43	460.5	24.7	2156	7	US-11-136-527-3843	Sequence 3843, Ap
44	459.5	24.6	3219	7	US-11-136-527-4059	Sequence 4059, Ap
45	459.5	24.6	3295	7	US-11-136-527-3736	Sequence 3736, Ap

ALIGNMENTS

RESULT 1

US-11-028-922A-4
; Sequence 4, Application US/11028922A
; Publication No. US20050271639A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Marc
; TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
; FILE REFERENCE: CCP-7019
; CURRENT APPLICATION NUMBER: US/11/028,922A
; CURRENT FILING DATE: 2005-01-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-028-922A-4

Alignment Scores:
Pred. No.: 2,97e-189 Length: 1050
Score: 1744.50 Matches: 338
Percent Similarity: 96.61% Conservative: 4
Best Local Similarity: 95.44% Mismatches: 7
Query Match: 93.44% Indels: 5
DB: 7 Gaps: 1

US-09-367-052-2 (1-359) x US-11-028-922A-4 (1-1050)

QY 6 ValSerIleTyrThrSerAspAsnYrSerGluValGlySerGlyAspTyrAspSer 25
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DB 1 ATGGAATATACACTTCGATTAACCTACTCGAGAGAGTAGGCTCTGGAGACTATGACTCC 60

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QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 61 ACAAGGAACCTTCTCCGGGATGAAACGAAACTTCAACAGGATCTTCTGCCACC 120
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
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QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
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QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
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RESULT 2

US-11-136-527-2630
; Sequence 2630, Application US/11136527
; Publication No. US2005028750A1
; GENERAL INFORMATION:

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; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2630
; LENGTH: 1651
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-2630

Alignment Scores:
Pred. No.: 2,8e-188
Score: 1738.50
Percent Similarity: 96.33%
Best Local Similarity: 95.20%
Query Match: 93.12%
DB: 7
Gaps: 1

US-09-367-052-2 (1-359) x US-11-136-527-2630 (1-1651)

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DB 826 GTCGTGCACRAGTGATCTCCATCAGGAGGCCCTCGCCTTCTCCACTGTTCGCTGAAC 885
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
DB 886 CCCATCTCTACGCCCTTCTCTCGGGGCCAAATTCAGAGCTCCGCGCAGCATGCACCTCAAT 945
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
DB 946 TCCATGAGCAGAGCTCCAGCCTCAAGATCTTCCAAAGGGAACGGGTGGACACTCT 1005
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
DB 1006 TCCGTCTCCACAGTCAGATCTCTCAAGTTTCACTCCAGC 1047

RESULT 3
US-10-955-054A-112
; Sequence 112, Application US/10955054A
; Publication No. US20050266420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAL, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AYERS, MARK
; APPLICANT: SPEC. JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTXC:880US
; CURRENT APPLICATION NUMBER: US/10/955, 054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 1225
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-112

Alignment Scores:
Pred. No.: 1.32e-181 Length: 1225
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 6 Gaps: 1

US-09-367-052-2 (1-359) x US-10-955-054A-112 (1-1225)

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
DB 35 ATCAGTATATACATCTTCAAGTAACTACTACCGAGGAAATGGGCTCAGGGAGCTATGACTCC 94
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 95 ATGAAGGAACCCCTGTTTCGTGGAAGAAATGCTAAATTTCAATAAATCTTCCTGCCACC 154
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
DB 155 ATCTACTCCATCATCTCTTAACTGGCAATGTGGCAATGGATGGTTCATCTCTGGTCATG 214
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
DB 215 GGTTACAGAAGAACTGAGAAGCATGACGACAGTACAGGCTGCACCTGTGCTAGTGGCC 274

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QY 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
DB 275 GACCTCTCTTGTGTATCATCGCTTCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC 334
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
DB 335 TTTGGGAACCTTCTATGCAAGGCGTCCATGTCTATCACAGTCAACCTCTACAGCAGT 394
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
DB 395 GTCCTCATCTCGCCTTTCATAGTGGACCGCTACGTGGCCATCGTCCACGCCACCAAC 454
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
DB 455 AGTCAGAGCCCAAGGAAGCTGTGGCTGAAAAGGTCTATGTGGCGTCTGGATCCCT 514
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
DB 515 GCCTCTCTGCTGACTATTCCTGACCTTCATCTTTCGCAACGTC-----AGT 559
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
DB 560 GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGGTGTG 619
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
DB 620 TTCCAGTTTTCAGCACATCATGTGGTGGCTTATCTCTGCTGGTATGCTATCTCTCTGTC 679
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 680 TATTGCAATTATCATCTCCAGCTGTCTCACTCCAGGGCCACCAAGGCGCAAGGCCCTC 739
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
DB 740 AAGACCACAGTCATCTCTCTGCTTCTTCTGCTGCTTCTGCTGCTTCTTACTACTATGGG 799
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
DB 800 ATCAGCATCGACTCTCTTCTCTCTGGAATATCATCAAGCAAGGGGTGTGAGTTTGAAC 859
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 860 ACTGTGCACAGTGGATTTCCATCACCAGGGCCCTAGCTTTCTTCCACTGTGTCTGAAAC 919
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
DB 920 CCCATCTCTATGCTTCTCTTGGAGCCAAATTTAAACCTCTGCCCGCAGCAGCTCACC 979
QY 326 SerMetSerArgGlySerSerLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
DB 980 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCTCTTCCAAAGGAAGCGAGGTGGACATTCA 1039
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
DB 1040 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCAGC 1081

RESULT 4
US-11-028-922A-3
; Sequence 3, Application US/11028922A
; Publication No. US20050271639A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Marc
; TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
; FILE REFERENCE: CCP-7019
; CURRENT APPLICATION NUMBER: US/11/028, 922A
; CURRENT FILING DATE: 2005-01-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-028-922A-3

```

Alignment Scores:									
Pred. No.:	2.07e-181	Length:	1662						
Score:	1678.50	Matches:	319						
Percent Similarity:	95.48%	Conservative:	19						
Best Local Similarity:	90.11%	Mismatches:	11						
Query Match:	89.90%	Indels:	5						
DB:	7	Gaps:	1						
US-09-367-052-2 (1-359) x US-11-028-922A-3 (1-1662)									
QY	6	ValSerIleTyrThrSerAspAnfYrSerGluGluValGlySerGlyAspTyrAspSer	25						
DB	63	ATCAGTATATACATTCAGATTAACATACACCGAGAAATGGGCTCAGGGACTATGACTCC	122						
QY	26	AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr	45						
DB	123	ATGAAGGAACCCCTGTTCCGTGAAGAAATGCTAATTTCAATAAAATCTTCTGCCAC	182						
QY	46	IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet	65						
DB	183	ATCTACTCCATCATCTTCTTAAGTGGCAATGGATGGTGGTGGTGGTGGTGGTGG	242						
QY	66	GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla	85						
DB	243	GGTTACCAGAAACATGAGAACGATGACGACAGTACAGGCTGCACCTGTCTGAGTGG	302						
QY	86	AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr	105						
DB	303	GACCTCTCTTTGTGTCATCAGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGG	362						
QY	106	PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer	125						
DB	363	TTTGGGAATCTTCTATGCAAGGAGTCCATGTCATCTACACAGTCAACCTCTACAGC	422						
QY	126	ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn	145						
DB	423	GTCTCATCTCTGGCCCTTCATCAGTCTGGACCGCTACTTGGCCATCTGCCCGCCAC	482						
QY	146	SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro	165						
DB	483	AGTCAGAGGCCAAGGAAGCTGTGGCTGAAAAGGTGCTATGTTGGCGTCTGGATCC	542						
QY	166	AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer	185						
DB	543	GCCTCTCTGCTGACTATTCGCGACTTCATCTTTGCCAAGCTC-----AGT	587						
QY	186	GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal	205						
DB	588	GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGTGGTGT	647						
QY	206	PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys	225						
DB	648	TTCCAGTTTTCAGCACATCATGTTGGCCCTTATCTGCTGGTATTGTCATCTCTCTGC	707						
QY	226	TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu	245						
DB	708	TATTTGATATATCATCTCCAAAGCTGTACACTCCAGAGGCCACAGAGCGCAAGCCCT	767						
QY	246	LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly	265						
DB	768	AAACACACAGTCATCTCATCTCTGGCTTCTTCTGGCTGTGGCTGTCTTACTACATTGG	827						
QY	266	IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer	285						
DB	828	ATCAGCATCGACTCTTCTATCTCTCTGGAAATCATCAAGCAAGGGTGTGAGTTTGA	887						
QY	286	IleValHisIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	305						
DB	888	ACTGTGCACAAAGTGGATTTCCATCACCGAGGCCCTAGCTTCTTCCACTGTGTCTGA	947						
QY	306	ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn	325						
DB									
US-10-955-054A-141									
; Sequence 141, Application US/10955054A									
; Publication No. US20050266420A1									
; GENERAL INFORMATION:									
; APPLICANT: PUSZTAI, LAJOS									
; APPLICANT: SYMMANS, W. FRASER									
; APPLICANT: HESS, KENNETH R.									
; APPLICANT: AYERS, MARK									
; APPLICANT: STEC, JAMES									
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY									
; FILE REFERENCE: UTXC:880US									
; CURRENT APPLICATION NUMBER: US/10/955,054A									
; CURRENT FILING DATE: 2004-09-30									
; NUMBER OF SEQ ID NOS: 195									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 141									
; LENGTH: 8747									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-955-054A-141									
Alignment Scores:									
Pred. No.:	1.15e-179	Length:	8747						
Score:	1672.50	Matches:	318						
Percent Similarity:	95.20%	Conservative:	19						
Best Local Similarity:	89.83%	Mismatches:	12						
Query Match:	89.58%	Indels:	5						
DB:	6	Gaps:	1						
US-09-367-052-2 (1-359) x US-10-955-054A-141 (1-8747)									
QY	6	ValSerIleTyrThrSerAspAnfYrSerGluGluValGlySerGlyAspTyrAspSer	25						
DB	4862	TTGCAGATATACATTCAGATTAACATACACGAGAAATGGGCTCAGGGACTATGACTCC	4921						
QY	26	AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr	45						
DB	4922	ATGAAGGAACCCCTGTTTCCGTGAAGAAATGCTAATTTCAATAAAATCTTCTGCC	4981						
QY	46	IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet	65						
DB	4982	ATCTACTCCATCATCTTCTTAAGTGGCAATGGATGGTCACTCTGTCATGTCATG	5041						
QY	66	GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla	85						
DB	5042	GGTTACCAGAAACATGAGAACGATGACGACAGTACAGGCTGCACCTGTCTGAGTGG	5101						
QY	86	AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr	105						
DB	5102	GACCTCTCTTGTGTCATCGCTTCCCTTCTGGCAGTTGATGCCGTGGCAAACTGGT	5161						
QY	106	PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer	125						
DB	5162	TTTGGGAATCTTCTATGCAAGGAGTCCATGTCATTTACACAGTCAACCTCTACAG	5221						
QY	126	ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn	145						
DB	5222	GTCTCATCTGGCCCTTTCATGCTGGACCGCTACCTGGCCATCTGCCGCCAAC	5281						
QY	146	SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro	165						
DB	5282	AGTCAGAGCCCAAGGAAGCTTGTGGCTGAAAAGGTGCTATGTTGGCGTCTGGATCC	5341						


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QY 166 AlaLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
D 5342 GCCCTCTGCTGACTATTCCTCCGACTTCATCTTTGCCAACGTC-----AGT 5386
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
D 5387 GAGGAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGTG 5446
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
D 5447 TTCAGTTTCAGACATCATGTTGGCTTATCTGCTGCTGATTTGTCATCTCTGCTGC 5506
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
D 5507 TATTGCAATATCATCTCCAAGCTGTCCACTCCCAAGGGCCACCAGAAGCGCAAGGCCCTC 5566
QY 246 LysThrThrValIleLeuIleAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
D 5567 AAGACACAGTCATCTCATCTGCTGCTTCTTCCGCTGTTGGCTTACTACTATTTGG 5626
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
D 5627 ATCAGCATCAGCTCTCTCATCTCTGGAATCATCAAGCAAGGTGTGAGTTGAGAAC 5686
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
D 5687 ACTGTGCACAAGTGGATTTCCATCAGCGGCTAGCTTCTTCCACTGTTGCTGAAC 5746
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
D 5747 CCATCTCTATGCTTCTCTTGGAGCCAAATTTAAACCTCTGCCCGACGCACTCACC 5806
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
D 5807 TCTGTGAGCAGAGGGTCCAGCTCAGATCTCTCCAAAGAAAGCGAGGTGACATTCA 5866
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
D 5867 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 5908

RESULT 6
US-10-955-054A-121
; Sequence 121, Application US/10955054A
; Publication No. US20050266420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SWAMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AYERS, MARK
; APPLICANT: STEC, JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTXC:890US
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 1102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-121

Alignment Scores:
Pred. No.: 9,32e-181 Length: 1102
Score: 1670.50 Matches: 317
Percent Similarity: 95.20% Conservative: 20
Best Local Similarity: 89.55% Mismatches: 12
Query Match: 89.48% Indels: 5
DB: 6 Gaps: 1

US-09-367-052-2 (1-359) x US-10-955-054A-121 (1-1102)
```

RESULT 7

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QY 6 ValSerIleTyrThrSerAspAenTyrSerGluGluValGlySerGlyAspTyrAspSer 25
D 53 ATCAGTATATATACACTTTCAGATACTACACCGAGAAATGGGCTCAGGGGACTATGACTCC 112
QY 26 AsnLysGluProCysPheArgAspGluAsnValIlePheAsnArgIlePheLeuProThr 45
D 113 ATGAGGAACCCCTGTTTCCGTGAAGAAATGCTATTTTCAATAAATCTTCTCGCCACC 172
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
D 173 ATCTACTCCATCATCTTCTTAACTGGCAATGATGGTGGTTCATCTCGTTCATG 232
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
D 233 GGTATTACAGAAGAAATGAGAGCATGACGACAAAGTACAGGCTGCACCTGTGAGTGCC 292
QY 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
D 293 GACCTCTCTTGTGTCATCAGCTTCCCTTCTGGGCAAGTGTATGCCGTGGCAAACTGGTAC 352
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
D 353 TTTGGGAACCTTCTATGCAAGGCAGTCCATGTCTACACAGTCAACCTCTACAGCAGT 412
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrIleAlaIleValHisAlaThrAsn 145
D 413 GTCTCTCATCTGCGCTTTCATCAGTCTGGACCGCTACCTGCGCAATGTGCCACGCCAAC 472
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrIlePro 165
D 473 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAGGTGTCTATGTTGGCTGTGATCCCT 532
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
D 533 GCCCTCTCTGCTGACTATTCCTCGACTTCATCTTTGCCAACGTC-----AGT 577
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
D 578 GAGGAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGTG 637
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
D 638 TTTCCAGTTTCAGACATCATGTTGGCTTATCTGCTGCTGATTTGTCATCTCTGCTGC 697
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
D 698 TATTGCAATATCATCTCCAAGCTGTCCACTCCCAAGGGCCACCAGAAGCGCAAGGCCCTC 757
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
D 758 AAGACCAATATCATCTCCCTGCTGCTTCTTCTGCTGTTGGCTGCTTACTACTATTGG 817
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
D 818 ATCAGCATGACTCTCTTCTCTCTGGAATCATCAAGCAAGGTGTGAGTTTGAAGAAC 877
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
D 878 ACTGTGCACAAGTGGATTTCCATCAGCGGCTTACTGCTTCTTCCACTGTTGCTGAAC 937
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
D 938 CCCATCTCTATGCTTCTTCTTGGAGCCAAATTTAAACCTCTGCCCGACGCACTCACC 997
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
D 998 TCTGTGAGCAGAGGGTCCAGCTTCAAGATCTCTCCAAAGAAAGCGAGGTGACATTCA 1057
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
D 1058 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1099
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Db 182 AGAAGCTGCTGGCTGAAAGCGCTCTATGTGGGTCTCGATCCCCCGCCCTCCCTCTG 241
Qy 170 ThrIleProaspPheIlePheAlaAspValSerGlnGlyAspIleSerGlnGlyAspAsp 189
Db 242 ACTATCCCTGACATCATCTTCCGCGATGTC-----AGCCAGGGGGAGCGGC 286
Qy 190 ArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValValPheGlnPheGln 209
Db 287 AGGTATACATCTGTGACCGCCTTTACCCCGACAGCGCTGTGGATGGTGTTCACAGTTCCAG 346
Qy 210 HistMetValGlyLeuIleLeuProGlyIleValIleLeuSerCysTyrCysIleIle 229
Db 347 CACATCATGTGGGTCTCATCTCCGCGGCATCGTCATCTGCTGCTTACTGATCATC 406
Qy 230 IleSerIleLeuSerHisSerIleGlyHisGlnLysArgLysAlaLeuLysThrVal 249
Db 407 ATCTCCAAGCTGTACACTCCAGGGCCACAGAGCGCAAGGCCCTCAAGACTACGGTC 466
Qy 250 IleLeuIleLeuAlaPhePheAlaCysTyrProTyrLeuProTyrTyrValGlyIleSerIleAsp 269
Db 467 ATCTTATCTGCTGCTTCTTGTGCTGTGCTACCGTATTTACGTGGGATCAGCATCGAT 526
Qy 270 SerPheIleLeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHisLys 289
Db 527 TCCTTATCTCTTTGGAGGTCATCAAGCAAGGATGTGAGTTCAGAGCGCTCGTGCAACRAG 586
Qy 290 TrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuLeuAsnProIleLeuTyr 309
Db 587 TGATCTCCATCATCAGGAGCCCTCGCTTCTTCCATCTGTGCTGAACCCCATCTCTAC 646
Qy 310 AlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsnSerMetSerArg 329
Db 647 GCCTTCTCGGGCCAAATTCAGAGCTCCGCGCAGCATGCACCTCAATTCATGAGCAGA 706
Qy 330 GlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSerSerValSerThr 349
Db 707 GGCTCAGCCCTCAAGATCCTTTCCAAAGGGAAACGGGGTGACACTCTCCCGTCTCCACA 766
Qy 350 GluSerGluSerSerPheHisSerSer 359
Db 767 GACTCAGATCCTCAAGTTTTCATCCAGC 796

RESULT 9

US-11-136-527-4204
; Sequence 4204, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4204
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4204

Alignment Scores:			
Pred. No.:	1.48e-134	Length:	1400
Score:	1268.00	Matches:	255
Percent Similarity:	89.55%	Conservative:	2
Best Local Similarity:	88.85%	Mismatches:	8
Query Match:	67.92%	Indels:	22
DB:	7	Gaps:	3

US-09-367-052-2 (1-359) x US-11-136-527-4204 (1-1400)

Qy 73 SerMetThrAspLysTyrArgLeuHisLeuSerValAlaAspLeuLeuPheValIleThr 92
Db 2 AGCATGACAGACAAAGTACCGGCTGCACCTGTCCGTGCTGACCTCTTTTGTGCATCACA 61
Qy 93 LeuProPheTrpAlaValaAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys 112
Db 62 CTCCTTC-----AGTGACGCCATGGCTGACTGTGTACTTTGGGAAATTTTATGTAAG 115
Qy 113 AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIleLeuAlaPheIle 132
Db 116 GCTGTGCATATCATCTACACCGTCAACCTTTACAGCAGTGTCTCATCTCGGCTTCATC 175
Qy 133 SerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGlnArgProArgLysLeu 182
Db 176 AGCCTGGACCGCTACCTTCCCATTTGTCCACGCCACCAACAGCCAGCGAGGAAAGCTG 235
Qy 153 LeuAlaGluLysAlaValTyrValGlyValTyrIleProAlaLeuLeuThrIlePro 172
Db 236 CTGGCTGAAAGAGCC----- 250
Qy 173 AspPheIlePheAlaAspValSerGlnGlyAspIleSerGlnGlyAspAspArgTyrIle 192
Db 251 GACATCATCTTCCCGCATGTC-----AGCCAGGGGGACGCGCAGGTACATC 295
Qy 193 CysAspArgLeuTyrProAspSerLeuTyrMetValValPheGlnPheGlnHisIleMet 212
Db 296 TGTGACCGCTTTTACCCGACACCTGTGGATGGTGTTCAGTTCAGACACATCATG 355
Qy 213 ValGlyLeuLeuProGlyIleValIleLeuSerCysTyrCysIleIleIleSerLys 232
Db 356 GTGGGTCTCATCTGCGGGCATCGTCATCTCTGTCTGTACTGCATCATCATCTCCAG 415
Qy 233 LeuSerHisSerLysGlyHisGlnLysArgLysAlaLeuLysThrThrValIleLeuIle 252
Db 416 CTGTCACTCTCCAGGGCCACAGAGCCAGGCCCTCAAGACTACGGTCACTCTTATC 475
Qy 253 LeuAlaPhePheAlaCysTrpLeuProTyrTyrValGlyIleSerIleAspSerPheIle 272
Db 476 CTGGCTTCTTGTGCTGCTGGCTACCGTATTACGTGGGATCAGCATCGATTCTTTCATC 535
Qy 273 LeuLeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHisLysTrpIleSer 292
Db 536 CTTTGGAGGTTCATCAAGCAAGATGTAGTTCGAGAGCGTCGTGCACAGTGGATCTCC 595
Qy 293 IleThrGluAlaLeuAlaPhePheHisCysCysLeuAsnProIleLeuTyrAlaPheLeu 312
Db 596 ATCAGGAGGGCTCTCGCTTCTTCCACTGTGCTGTAACCCCATCTCTACGGCTTCTC 655
Qy 313 GlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsnSerMetSerArgGlySerSer 332
Db 656 GGGGCCAAATTCAGAGASSTCCGCGCAGCATGCACCTCAATTCATGACGAGAGGCTCCAGC 715
Qy 333 LeuLysIleLeuSerLysGlyLysArgGlyGlyHisSerSerValSerThrGluSerGlu 352
Db 716 CTCAGATCCTTTCCAAAGGGAAACGGGGTGACACTCTTCCGTCTCCACAGAGTCAGAA 775
Qy 353 SerSerSerPheHisSerSer 359
Db 776 TCTCAAGTTTTCATCTCCAGC 796
RESULT 10
US-11-136-527-153
; Sequence 153, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294

```
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 153
; LENGTH: 1680
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-153

Alignment Scores:
Pred. No.: 2,5e-57 Length: 1680
Score: 594.00 Matches: 123
Percent Similarity: 54.60% Conservative: 67
Best Local Similarity: 35.34% Mismatches: 138
Query Match: 31.82% Indels: 20
DB: 7 Gaps: 4

US-09-367-052-2 (1-359) x US-11-136-527-153 (1-1680)

QY 17 GluValGlySerGlyAspTyrApp-----SerAanLysGlu 28
DB 209 GAAACAGACATCTCCCTACGATTATGGGAAAMRAAARMAMMMCTGACTCCCCG 268

QY 29 ProCyPheArgAspGluAanValHisPheAsnArgIlePheLeuProThrIleTyrPhe 48
DB 269 CCTGCCCCACAGGACTTCAGCCTGAACCTTGACAGAACCTTCTGCCAGTCCCTACAGC 328

QY 49 IleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMetGlyTyrGln 68
DB 329 CTCCTCTTTTGTGGGCTGTAGCAATGGGCGAGTGTCTGTCTACTACTAGAGCCAG 388

QY 69 LysLeuLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAlaAspLeuLeu 88
DB 389 CGCAGTCCCTGAGCAGCAGACACCTCTCTGCTCCACCTGGCTGTGGCGAGTACTG 448

QY 89 PheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTyrPheGlyLys 108
DB 449 CTGGTACTAACCTCCACCTGCTGGCAGTAGATGCTCTGCCCGAGTGGTTCGCGCTCT 508

QY 109 PheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuLe 128
DB 509 GGTCTCTGCAAGTGGCAGGTGGCCCTGTTCAACATCAACTTCTACGAGGCGCTTCCTG 568

QY 129 LeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGlnArg 148
DB 569 CTGGCTGTATAAGCTTTGACCTACCTAGCATAGTGTGATGCCACCCAGATCTACCGC 628

QY 149 ProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIleProAlaLeuLeu 168
DB 629 AGGAGCCCTGGGTAGCTGTAGCCCTCACCTGCATTGTTGTGGGTCTCTGTGTGCTC 688

QY 169 LeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSerGlnGlyAsp 188
DB 689 TTTGGCCCTCCAGATTTCATCTCTCTGTCAGCCAGCCAT-----GATCAGCGCTC 739

QY 189 AspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnPhe 208
DB 740 AATGCCACCATTCGCCAGTACAACCTCCCA--CAGGTGGGTGGAGTGTCTGTGGTGTA 796

QY 209 GlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCysTyrCysIle 228
DB 797 CTGCAGTAGTGGTGGTCTTCGTGATGCCCTTCTAGTCTAGTCTAGTCTAGTCTAGTCC 856

QY 229 IleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeuLysThrThr 248
DB 857 ATCTGTGCTGTGCTGTGCTGTCCAGAGGCGCAGAGGCGCTTTCAGAGTATGAGCTAGT 916

QY 249 ValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTrpValGlyIleSerIle 268
DB 917 GTGGTGGTGGTGGGCTTTGGCTGTCTGAGACCCCTTATCACCTGGGTGGTGGTGTAGT 976

QY 269 AspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHis 288
DB 977 GATATCTTTATGAGCTGGGAGTTCCTGGCCGCAAACTGTGTGCGAAGAACCATGTGGAC 1036

QY 289 LysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsnProIleLeu 308
DB 1037 GTAGCAAGTCTAGTCACCTCAGGCATGGGCTACATGCACTGTCTGCTCAATCCACTGCTC 1096

QY 309 TyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsnSerMetSer 328
DB 1097 TATGCTTTGTGGAGTGAAGTTCAAAGAACAAATGTGGATGTGCTCATGCGCCTGGGC 1156

QY 329 ArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSerSerValSer 348
DB 1157 CGCTCTGAC-----CAGAGAGGMCAGGAGCGGAGCGGCGCTTCA 1192

QY 349 ThrGluSerGluSerSerSerPhe 356
DB 1193 TCTTCAGGAGAGAAATCATCTGG 1216

RESULT 11
US-11-136-527-4249
; Sequence 4249, Application US/111136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4249
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4249

Alignment Scores:
Pred. No.: 2,2e-55 Length: 1400
Score: 576.00 Matches: 117
Percent Similarity: 55.86% Conservative: 64
Best Local Similarity: 36.11% Mismatches: 131
Query Match: 30.85% Indels: 12
DB: 7 Gaps: 3

US-09-367-052-2 (1-359) x US-11-136-527-4249 (1-1400)

QY 33 AspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyrPheIleIlePheLeu 52
DB 1 GACTTCAGCTGNACTTTGACAGAACCTTCTGCCAGTCTCTACAGCCTCCTCTTTTG 60

QY 53 ThrGlyIleValGlyAsnGlyLeuValIleLeuValMetGlyTyrGlnLysLysLeuArg 72
DB 61 CTGGGCTGTAGGCAATGGGCGAGTGGTGTCTACTAGCCAGCGGCACTGCGCTG 120

QY 73 SerMetThrAspLysTyrArgIleHisLeuSerValAlaAspLeuLeuPheValIleThr 92
DB 121 AGCAGCAGACACACCTTCTGCTCCACCTGGCTGTGGCGAGTGTACTGTGGTACTAAC 180

QY 93 LeuProPheTrpAlaValAspAlaMetAlaAspTyrPheGlyLysPheLeuCysLys 112
DB 181 CTCCTACTGGGCGAGTAGTGTGCTGCCAGTGGGTTTCGGCTCTGTCTCTGCAAA 240

QY 113 AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIleLeuAlaPheIle 132
DB 241 GTGGCAGGTGGCTGTGTCAACATCAACTTCTACGAGGCGCTTCTGCTGGCTGTATA 300

QY 133 SerLeuAspArgTyrIleLeuAlaIleValHisAlaThrAsnSerGlnArgProArgLysLeu 152
DB 301 AGCTTTGACCGCTACCTAGCATAGTGTGATGCCACCCAGATCTACCGAGGAGCCCTGG 360
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QY 153 LeuAlaGluLysAlaValTyrValGlyValTyrPheLeuLeuLeuLeuThrllePro 172
Db 361 GTACGTGTAGCCCTCACCTGCATTGTGTGGGTCTCTGTGTCTTTGGCCCTCCCA 420
QY 173 AspPheIlePheAlaAspValSerGlnGlyAspIleSerGlnGlyAspArgTyrIle 192
Db 421 GATTTTCACTTCTGTGACGCCAT-----GATCAGGCGCTCAATGCCACCCAT 471
QY 193 CysAspArgLeuTyrProAspSerLeuTyrMetValValPheGlnPheGlnHisIleMet 212
Db 472 TGCCAGTACAACTTCCCA---CAGGTGGGTGGACTGCTGTGGGTACTGCAGCTAGTG 528
QY 213 ValGlyLeuLeuLeuProGlyIleValIleLeuSerCysTyrCysIleIleIleSerLys 232
Db 529 GCTGGTTTCTGTATGCCCTTCTAGTCAATGCTGTCTATGCCATATCCCTGGCTGTG 588
QY 233 LeuSerHisSerLysGlyHisGlnLysArgLysAlaLeuLysThrValIleLeuIle 252
Db 589 CTGCTGTCTCCAGAGCCAGAGCGCTTCGAGCTATGAGGTAGTGGTGGTGGTG 648
QY 253 LeuAlaPhePheAlaCysTyrLeuProTyrTyrValGlyIleSerIleAspSerPheIle 272
Db 649 GTGGCTTTGCTGCTGTGACCCCTATCACCTGTGTGTAGTGGATATCCTTATG 708
QY 273 LeuLeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHisLysThrIleSer 292
Db 709 GACGTGGAGTTTGGCCCGCAACTGTGTGCGAGAAAGCCATGTGACGTAGCAAGTCA 768
QY 293 IleThrGluAlaLeuAlaPhePheHisCysCysLeuAsnProIleLeuTyrAlaPheLeu 312
Db 769 GTCACTTCAGGATGGCTATGCTGCTGCTCAATCCTATGCTCTATGCTTGTG 828
QY 313 GlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsnSerMetSerArgGlySerSer 332
Db 829 GGAAGTGAAGTTCAAGAACAAATGTGATGTCTCATGCGCTGGCGCTCTGAC--- 885
QY 333 LeuLysIleLeuSerLysGlyLysArgGlyGlyHisSerSerValSerThrGluSerGlu 352
Db 886 -----CAGAGAGGCMCCGCGCGAGCAGCCTTTCATCTTCCACGGAGA 924
QY 353 SerSerSerPhe 356
Db 925 GAATCATCTCTGG 936

RESULT 12
US-11-136-527-2373
; Sequence 2373, Application US/111136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/111136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2373
; LENGTH: 1324
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2373

Alignment Scores:
Pred. No.: 8,09e-54 Length: 1324
Score: 562.00 Matches: 130
Percent Similarity: 53.10% Conservative: 67
Best Local Similarity: 35.04% Mismatches: 126
Query Match: 30.10% Indels: 48
DB: 7 Gaps: 10

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US-09-367-052-2 (1-359) x US-11-136-527-2373 (1-1324)
QY 12 AspAsnTyrSer---GluGluValGlySerGlyAspTyrAsp----- 24
Db 150 GATAATTTTCAGCCTTGAAGACTTCTTTTCAGTGGAGATATTGACAGTTTACAATTACAGTTCT 209
QY 25 -----SerAsnLysGluProCysPheArgAspGluAsnValHisPhe 38
Db 210 GACCCGCCCTTTTACTCTGTGCAGATGCTGCCCATATG---CCCTCAGCGAACCTTAGATATC 266
QY 39 AsnArgIlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAsn 58
Db 267 AACAGTATGCTGTGGTTCATATACGTTCTGGTGCATTTGCTGAGTCTCTGGTGGGGAAC 326
QY 59 GlyLeuValIleLeuValMetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyr 78
Db 327 TCCTGCTGATGCTGTGTCATCTGTGACAATCGAAGCACCTGCTCTGTTACCGACGCTTAC 386
QY 79 ArgLeuHisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheThrAlaVal 98
Db 387 CTGCTGAACCTGGCCATTCGTCATCTGTTCTTGGCCCTGACCTTGCTGTGGGTGCA 446
QY 99 AspAlaMetAlaAspTyrPheGlyLysPheLeuCysLysAlaValHisIleIleTyr 118
Db 447 TCTAAAGTAAATGGATGGATTTTGGCTCATCTCTGTGCAAGGATATTCGTTCTCGTCAG 506
QY 119 ThrValAsnLeuTyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeu 138
Db 507 GAGATTACCTTCTACAGCAGTGTCTGTGTTAGCTGCATCAGCATGACGACGCTACCTG 566
QY 139 AlaIleValHisAlaThrAsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaVal 158
Db 567 GCATCGTCCACGCCCAAGTACATGATCCAGAGAGACACTTGTGC---AAGTTTGTG 633
QY 159 TyrValGlyValTyrIleProAlaLeuLeuThrIleProAspPheIlePheAlaAsp 178
Db 624 TGCATCACCATTGGTTTCTCTACATGTTCTGCTCCCTGCCCATCTTCATCTT 677
QY 179 ValSerGlnGlyAspIleSerGlnGlyAspArgTyrIleCysAspArgLeuTyrPro 198
Db 678 -----CGGACTACTGTTAAAGCAACCTTCTACCGTAGTCTGC-----TATGAG 722
QY 199 Asp-----SerLeuTyrMetValValPheGlnPheGlnHisIleMetVal 213
Db 723 AATATAGGTAATAATACATCCAAAGTGGAGGTGGTACTCGCATCTCGCTCAGACCTAT 782
QY 214 GlyLeuIleLeuProGlyIleValIleLeuSerCysTyrCysIleIleIleSerLysLeu 233
Db 783 GGCTTCTCTGCTGCTGCTCATCATGCTGTCTGTATGGGTTCACACTGCGCAGCTC 842
QY 234 SerHisSerLysGlyHisGlnLysArgLysAlaLeuLysThrValIleLeuLeu 253
Db 843 TTTAAGGCCCATCGGGGAGAGACACCGGCGCATCGCGGTCTATCTTGTGTGGTCTC 902
QY 254 AlaPhePheAlaCysTyrLeuProTyrTyrValGlyIleSerIleAspSerPheIleLeu 273
Db 903 GTCTTCTGCTGCTGCTGCTTCCCTACACATTTGCTCTTTCACAGACACCTCATGAGA 962
QY 274 LeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHisLysThrIleSerIle 293
Db 963 ACCAAGCTGATCAAGAGGACCTGTGAACCCGAGACGAGATTAACAAAGCTTTGGAGCT 1022
QY 294 ThrGluAlaLeuAlaPhePheHisCysCysLeuAsnProIleLeuTyrAlaPheLeuGly 313
Db 1023 ACTGAGATTTTGGCTTCTCCACAGCTGCTTAACCCCATCATCTATGCTTTATTGGC 1082
QY 314 AlaLysPheLysSerSerAlaGlnHisAlaLeuAsnSerMetSerArgGlySerSerLeu 333
Db 1083 CAGAAATTTTCGC-----CATGGACTT-----CTC 1106
QY 334 LysIleLeuSerLys-----GlyLysArgGlyGlyHis 344
Db 1107 AAGATCATGGCTAAATTATGCGCTTGTCAAGAGGAGTTCTTATGCCAAGGAGGAGGCT 1166

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US-09-367-052-2 (1-359) x US-11-127-877-25 (1-3177)

QY 10 ThrSerAspAsnTyrSerGluValGlySerGlyAspTyr-----AspSerAenLys 27
:::|||||:::|||||:::
Db 306 TCCAGTGACGATATTATTTGGTCAGTCAGTCAATCTACTATTACTCAGTTGATCTGAGATG 365

QY 28 GluProCysPheArgaspGluAenValHisPheAsnArgIlePheLeuProThrIleTyr 47
:::|||||:::|||||:::
Db 366 TTACTGTGCCTCGCATGCGAGGTCAGCGAGTTCTCCAGGCTATTGTTACCGATTGCTTAC 425

QY 48 PheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMetGlyTyr 67
:::|||||:::|||||:::|||||:::
Db 426 TCCTTGATCTGTCTTGGCCCTCGGGGAATATCTGTGTGTGATCACCTTGTCTTTT 485

QY 68 GlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAlaAspLeu 87
:::|||||:::|||||:::|||||:::
Db 486 TATAAGAAGCCAGGCTATGACAGAGCGTCTATCTTGAACAATGCCATTCGACATC 545

QY 88 LeuPheValIleThrLeuProPheTrpAlaValAsp---AlaMetAlaAspTrpTyrPhe 106
:::|||||:::|||||:::|||||:::
Db 546 CTCTTTGTTCTTACTCTCCATTCGCGCAGTGAGTCATGCCACCGGTCGCGGTTTTTC 605

QY 107 GlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSerVal 126
:::|||||:::|||||:::|||||:::
Db 606 AGCAATGCCAGTCGAAAGTTGCTAAAAGGCATCTATGCCATCACTTAACCTGCGGGATG 665

QY 127 LeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAenSer 146
:::|||||:::|||||:::|||||:::
Db 666 CTGCTCTGATTCGATTAGCATGAGCCGATCATCGCCATGTACAGCGAGTAAGTCA 725

QY 147 -----GlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIle 164
:::|||||:::|||||:::|||||:::
Db 726 TTCGGGCTCGATCCAGAACACTACCAGCGCAGCAAATCATCTGCTTGTGTGGGG 785

QY 165 ProAlaLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIle 184
:::|||||:::|||||:::|||||:::
Db 786 CTGCTAGTCATCATCTCCAGCTCAACTTTTGTCTTC-----AACCAAAATACAAAC 836

QY 185 SerGlnGlyAspAspArgTyrIleCysAspArgLeuTyr-----ProAspSer 200
:::|||||:::|||||:::|||||:::
Db 837 ACCAAGGACGAT-----GTCTGTGAACCAAGTACAGACTGTCTCGGAGCCATC 890

QY 201 LeuTrpMetValValPheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIle 220
:::|||||:::|||||:::|||||:::
Db 891 AGGTGGAAGCTGCTGATGTTGGGCTTGAGCTACTCTTTGGTTCTTTATCTCTTGATG 950

QY 221 ValIleLeuSerCystTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln 240
:::|||||:::|||||:::|||||:::
Db 951 TTCATGATATTTGTTACAGTTCAATGTGCAAAACCTTGGTGCAAGCTCAGAAATCTAA 1010

QY 241 LysArgLysAlaLeuLysThrThrValIleLeuLeuAlaPhePheAlaCysTrpLeu 260
:::|||||:::|||||:::|||||:::
Db 1011 AGGCACAAAGCCATCCGTGTAATCATAGCTGGTGCTGTGTCTTGTGCTTGTGAT 1070

QY 261 ProTyrTyrValGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGly 280
:::|||||:::|||||:::|||||:::
Db 1071 CCTCATAACATGCTGCTGTGTGACGGCT---GCAAAATTTGGTAAATGAACCGATCC 1127

QY 281 CysAspPheGluSerIleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePhe 300
:::|||||:::|||||:::|||||:::
Db 1128 TGCCAGAGCGAAAGCTAATTTGGCTATACGAAACCTGTCCACAGAAGCTCTGCTTCTCTG 1187

QY 301 HisCysCysLeuAenProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerAla 320
:::|||||:::|||||:::|||||:::
Db 1188 CACTGTGCTGAACCTGTGCTACGCTTTTATTGGGGAAGTTC----- 1235

QY 321 GlnHisAlaLeuAenSerMetSerArgGlySerSerLeuLysIleLeuSer 337
:::|||||:::|||||:::|||||:::
Db 1236 -----AGAACTACTTTCTGAGAGTCTTTGAAGACCTGTGG 1271

QY 338 -----LysGlyLysArgGlyGlyHisSerSerValSerThrGluSerGluSer 353
:::|||||:::|||||:::|||||:::

Db 1272 TGTGTGAGAAAGAGTACAGTCTCTCAGGCTTCTCCTGTGCGGAGGTACTCAGAAAAAC 1331

QY 354 SerSerPheHisSerSer 359
:::|||||:::|||||:::
Db 1332 ATTTCTCGGCAGACAGT 1349

RESULT 15

US-10-995-561-13239

; Sequence 13239, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995.561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13239

; LENGTH: 30151

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-995-561-13239

Alignment Scores:

Pred. No.: 1,66e-48 Length: 30151

Score: 533.00 Matches: 119

Percent Similarity: 50.41% Conservative: 67

Best Local Similarity: 32.25% Mismatches: 151

Query Match: 28.55% Indels: 32

DB: 6 Gaps: 7

US-09-367-052-2 (1-359) x US-10-995-561-13239 (1-30151)

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGly----AspTyrAsp 24
:::|||||:::|||||:::|||||:::
Db 21124 ATCCAGGCTTTCCACATGATCAGTTCCCTGAAATCAGTCAGACAGAAAACTTTTGAGTAGCAT 21183

QY 25 SerAenLysGluProCysPheArgaspGluAenValHisPheAenArgIlePheLeuPro 44
:::|||||:::|||||:::|||||:::
Db 21184 GATTGGCTGAGGCTGTTATATTGGGACATCGTGTCTTTGGAGCTGTGTTCTGTCC 21243

QY 45 ThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAenGlyLeuValIleLeuVal 64
:::|||||:::|||||:::|||||:::
Db 21244 ATAATCTACTCCGTCATCTTTGCCATTGGCTGGTGGGAAATTTGTTGGTAGTGTGTTGCC 21303

QY 65 MetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerVal 84
:::|||||:::|||||:::|||||:::
Db 21304 CTCACCAACAGCAAGAGCCCAAGAGTGTCAACGACATTTACCTCTCGAACCTGCGCTTG 21363

QY 85 AlaAspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrp 104
:::|||||:::|||||:::|||||:::
Db 21364 TCTGATCTGCTGTTGTAGCCACTTTGCCCTCTCGAGCTCACTATTGATTAATGAAGAAG 21423

QY 105 TyrPheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSer 124
:::|||||:::|||||:::|||||:::
Db 21424 GGCCTCCACATGCCATGTGCAAAATTCATACCGCTTCTTCTTCATCGGCTTTTITGGA 21483

QY 125 SerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThr 144
:::|||||:::|||||:::|||||:::
Db 21484 AGCATATCTTCATCACCGCTCATCAGCATTCATAGGTACCTGGCCATCGTCTCGCGCGCC 21543

QY 145 AsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIle 164
:::|||||:::|||||:::|||||:::
Db 21544 AACTCCAATGAACAACCGGACCGTCGACGATGGCCTACCATCGCTAGGCGTCTGGGCA 21603

QY 165 ProAlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIle 184
:::|||||:::|||||:::|||||:::
Db 21604 CGAGCCATTTTGGTGGCAGCACCCCAGTTCATGTTTCACAAAGCAGAAAGAAATGA-- 21660

QY 185 SerGlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAsp-----SerLeu 201
:::|||||:::|||||:::|||||:::

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Db 21661 -----||| |||||:::
||| |||||:::
TGCCTTGGTGACTACCCCGAGGTCTCCAGGAAATC 21696
QY 202 TrpMetValValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleVal 221
||| |||||:::
21697 TGGCCGTGCTCGCAATGTGGAACAAATTTCTTGGCTTCCTACTCCGCCCTGCTCAAT 21756
QY 222 IleLeuSerCysTyrCysIleIleSerLysLeuSerHisSerLysGlyHisGlnLys 241
::: |||||
21757 ATGAGTATTGCTACTTCAGARTCATCCAGACGCTGTTTCTTGCAGAACACCAAGAAA 21816
QY 242 ArgLysAlaLeuLysThrThrValIleLeuIleAlaPhePheAlaCysTrpLeuPro 261
||| |||||:::
21817 GCCAAGCCATTAAACTGATCCTCTGGTGGTCATCGTGTCTTCTCTCGACACCC 21876
QY 262 TyrTyrValGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCys 281
||| |||||:::
21877 TACAACRTTATGATTTTCTCGAGAGCGTTAAGCTCTATGACTTCTTT---CCAGTTGT 21933
QY 282 AspPheGluSerIleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHis 301
||| |||||:::
21934 GACATGAGGAAGGATCTGAGGCTGGCCCTCAGTGTGACTGAGAYGGTTGCATTTAGCCAT 21993
QY 302 CysCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGln 321
||| |||||:::
21994 TGTGTCTGAATCCTCTCATCTATGCATTTGCTGGGGAGAGTTTCAGAGATACCTTTAC 22053
QY 322 HisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeu----- 336
||| |||||
22054 CACCTGTAT-----GGGAATGCCTGGCTGTCTGTGTGGCGCTCAGTC 22098
QY 337 -----SerLysGlyLysArgGlyGlyHisSerValSerThrGlu 350
||| |||||
22099 CACGTTGATTTCTCTCATCTGAATCACAAGGAGCGGCGATGGAAGTGTCTG----- 22152
QY 351 SerGluSerSerPheHisSerSer 359
||| ::: |||||
Db 22153 AGCAGCAATTTTACTTACCACACGAGT 22179
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Search completed: January 11, 2006, 02:49:02
Job time : 282 secs